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AF13739 Nephrosel
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AF220067 Drosophil
AC015209 Drosophil
AC01735 Drosophil
AE003823 Drosophil
L48441 Echinochloa
AL109850 S. pombe c
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AB007012 Spirochae
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Submitted (12-JUN-1996) Microbiology, Monash University, Wellington
Submitted (12-JUN-1996) Microbiology, Monash University, Wellington
Rd., Clayton, VIC 3168, Australia
Location/Qualifiers
1. 1481
/ Acqanism="Leptospira fainei"
/ Acranism="Hurstoridge"
/ Ab_xref="Laxon:48782"
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Adler, B., Chappel, R.J., Baranton, G., Bulach, D.M.,
Billinghurst, M.L., Letocart, M., Merien, F., Serrano, M.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFU60594 1481 bp DNA BCT 10-SEP-19
Leptospira fainei 16S ribosomal RNA gene, partial sequence.
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Pred. No. 3.9;
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
Bacteria; Labela, R.C., Cinco, M., Smythe, L.D., Symonds, M., Woo, T.H.S., Patel, B.K.C., Cinco, M., Smythe, L.D., Symonds, M., Noris, M. and Dohnt, M.
Identification of Leptonema by real-time homogeneous assay of rapid
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Leptospira interrogans strain 48/95 16S ribosomal RNA gene, partial
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Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun
Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun
Shin, Laboratory of Marine Molecular Microbiology, Faculty of
Shin, Laboratory of Marine Molecular Microbiology, Faculty of
Shin, Laboratory of Marine Molecular Microbiology, Faculty of Marine Molecular (State Microbiology)
Ryoto, Kyoto 306-01, Japan (E-mail:misun@kais.kyoto-u.ac.jp,
Tel:075-753-6224, Fax:075-753-6226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Science, Griffith University,
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Shin, M., Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A.
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(Insolrophic Lake)
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Unpublished
2. (Dases 1 to 283)
Woo, T.H.S. Patel, B.K.C., Cinco, M., Smythe, L.D., Symonds, M., Porris, M. and Dohnt, M.
Norris, M. and Dohnt, M.
Submitted (14-MY-1997) School of Science, Griffith Universitivance, QLD 4111, Australia
                                                                                                                                                                                                                                                           Spirochaeta sp. (sub_species:Freshwater obligate oligotroph, strain:FO-95) DNA.
Spirochaeta sp.
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( Jases 1 to 354)
Shin,M.-S.
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/db_xrefe"taxon:28185"
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AB007014 354 bp DNA BCT
Spirochaeta sp. 16S rRNA gene, partial sequence.
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/strain="48/95"
/db_xref="taxon:173"
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Best Local Similarity 95.5%;
Matches 21; Conservative (
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1 (bases 1 to 288)

Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Science, Griffith University,
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1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Leptcospira inadai 16s ribosomal RNA gene, partial sequence.
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Woo, T.H.S., Smythe, L.D., Symonds, M., Norris, M., Dohnt, M.,

Brenner, D.J., and Patel, B.K.C.

Direct Submission

Submitted (24-MAR-1997) School of Science, Griffith University and Patellia Australia

Location/Qualifiers
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/strain="79/95"
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Best Local Similarity 90.9%;
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Leptospira inadai 16s ribosomal RNA gene, partial sequence.
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Leptospira inadai 16s ribosomal RNA gene, partial sequence.
U94977
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S Woo'T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
L Submitted (24-MAR-1997) School of Science, Griffith Universit Brisbane, QLD 4111, Australia
Location/Qualifiers
1. 288
| Cognism="Leptospira inadai" | Astrain="346/95" |
E 2 (bases 1 to 288)
S Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct.Submission
L. Submitted (24 MAR-1997) School of Science, Griffith Universit
Brisbane, QLD 4111, Australia
Location/Qualifiers
1. 288
Location/Qualifiers
1. 288
/strain="Leptospira inadai"
/strain="Reptospira"
/strain="Reptospira"
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Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
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90.9%;
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Best Local Similarity 90.9%;
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01-JAN-1998 sequence.

us-09-380-826a-2.rge

ORGANISM

KEYWORDS

/ERSION SOURCE REFERENCE AUTHORS source

FEATURES

TITLE JOURNAL

AUTHORS

JOURNAL REFERENCE

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BASE COUNT ORIGIN

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Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Shin, Laboratory of Marine Molecular Microbiology, Faculty of Agriculture, Kyoto University; Oiwakecho, Kitashirakawa, Sakyoku, Kyoto, Kyoto 306-01, Japan (E-mail:misun@kais.kyoto-u.ac.jp, Tel:075-753-6224, Fax:075-753-6226)
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submission
Submitted (24-MR-1997) School of Science, Griffith University,
Brisbane, QLD 4111, Australia
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Spirochaeta sp. (sub_species:Freshwater obligate oligotroph.
strain:SO-104) DNA.
Spirochaeta sp.
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1 (bases 1 to 200)
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Leptospira inadai 16S ribosomal RNA gene, partial
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/organism="Leptospira inadai"
/strain="1078 VRI"
/db_xref="taxon:29506"
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.

1 (bases 1 to 288)
Woo,T.H.S., Smytho,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MR-1997) School of Science, Griffith University,
Brisbane, QDD 4111, Australia
Location/Qualifiers
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1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadal by continuously monitoring
fluorescence during rapid cycle PCR
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Leptospira inadai 16s ribosomal RNA gene, partial sequence.
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M., Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MAR-1997) School of Science, Griffith Universibane, QLD 4111, Australia
Location/Qualifiers

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Pred. No. 1.4e+02;
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Best Local Similarity 90.9
Matches 20; Conservative
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BASE COUNT ORIGIN

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TUDVLYQAGYYASINSEKYPLGGTYTALQNAFHTTPEVYCKRDAIDEIRICFYKDFKPRD
CVGSODLTSRKSCRYVLYSPFYPLGGAMVLKMPTEREAL"
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YCRGTRHCCSKNACCRGSDAPTQFTIHGLWPDYNDGSWPSCCYRSDFKEKEISTLMDG
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Proc. Natl. Acad. Sci. U.S.A. 90 (11), 5118-5122 (1993)
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                                                                                                             /sub_species="Freshwater obligate oligotroph"
/db_xref="taxon:28185"
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                      /organism="Spirochaeta sp."
/strain="SO-104"
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/db_xref="G1:289210"
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.orn.igo/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://arthur.epm.orn.i.gov/pub/xgrail), searches of the (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TiGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by the most of their length are predicted by the protein or EST similarity. Contact of their length are predicted by the sum of the protein or EST similarity of the protein or EST similarity. The protein of the protein or EST similarity of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are hitch the protein or EST similarity or the protein or EST similarity or the protein or EST similarity. The protein or EST similarity or the protein or EST similarity or the protein or EST similarity. The protein or EST similarity or the protein or EST similarity or the protein or EST similarity. The protein or EST similarity or the protein or EST similarity or the protein or EST similarity.
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I (bases I to 72590)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujil,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V. Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo, H., Moffat, K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:2642152. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
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Arabidopsis thaliana chromosome II section 214 of 255 of the complete sequence. Sequence from clones T517, AC003000 AE002093
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    .72590
    /organism="Arabidopsis thaliana"
/cultivar="Columbia"

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RVPIICTGNDFSTLYAPLIRDGRMEKFYWAPTREDRIGVCKGIFFTDKIKDEDIVTLV
DOFPGOSIDIFFGALRARVYDDEVNKFVESLGVEKIGRRLVNSREGPPVFEOPEMTYEK
LAFGGNALVMEDENVKRVDAETYLSQALGDANADAIGRGTFYGKTEEKEPSK"
complement(17561. 17639)
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join(418783. 18921.19188. 19352,19496. 19674,19766. 19861,
join(418783. 20034,20131. 20261,20593. >21237)
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join(18783. 18921.19188. 19352,19496. 19674,19766. 19861,
19965. 20034,20131. 20261,20593. 21237)
/gene="At2g39740"
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/gene="At2g39750"
complement(21380. >>24814)
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IGINGGKGGGKSFQCELVMAKMGINPIMMSAGELESGNAGEPAKLIRGRKYREAADLIK
AQSNKKSNGSFKVLAVKEDKQTDGDRWRGLAYDTSDDQQDITRGKGMVDSVFQAPMGT
GTHHAVLSSYEXVSQGLRQYNLDNMMDGFYIAPAFMDKLVVHITKNFLTLPNIKVPLI
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DOPEGGSIDFPEGALRARVYDDEVRKFYESLGYEKIGKRLYNSRGEPPVEQPEMTYEK
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CTDPVARENFDPTARSDDGTCVYNF
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14651 .14736,14836. .14941,15033. .15349,15834. .15878))
/gene="At2g39730"
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                                                                                                                                                                                                                                                /note="alternative splice form 2 GP/166835/M86720"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 85;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNSARPPSKIPSQGGQIWRPRHEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 35807 TGTTGGTTCACAAGATTTGACA 35828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                            /codon_start=1
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Best Local Similarity
Matches 20; Conserv
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KEYWORDS
SOURCE
ORGANISM
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AF165146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFTTTTTTOHRSPTREPPSSSSSPPSASMHADNSPTPTIVTRTRSNRSPNPVIVLRG
SAAAPSSDVVSEGLDRSAFOMYYDDGTDSGLRPLPPSMTEFLLGSGFDRLLDQISQIE
LNTNRNLRSCEHPPASKSAIEALPLIEIDPTHLLSDSQSHCAVCKENFVLKSSAREMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNHIYHPDCILPWLAIRNSCPVCRHELPAEDLTDGTGAALTAVTATAEEEEDSAAGLT
IWRLPGGGFAVGRIPGGWRGGDRMMPVVYTEVDGGRLGDERLPRRVAWGSRRGGRDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="T5I7.3"
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FVIGSVTRFGTLFGCMDSGLSSNSEEDAKSYGLMRINGSFSFYNDATSIEGNLAHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDSSGFLLLGDASYSWLGPTQYTPLVLQSTPLPYFDRVAYTVQLEGIRVGSKILSLPK
SVFVPDHTGAGQTMVDSGTQFTFLMGPVYTALKNEFITQTKSVLRLVDDPDFVFQGTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MASGSYWCYSCSRFVWVSDSISCPDCDGGFLELIQEPLDFTPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(13323. .13599,13713. .14005,14087. .14559,
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complement(4584. >5909)
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complement(<10039, .11304)
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                                                                                                                                                      .1024)
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                                                                                                                                                                                               complement(1266.
                                                                                                                                                  complement(1000
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us-09-380-826a-2.rge

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  The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral
                                                                                                  2 (bases 1 to 200799)
Turmel,M., Otis,C. and Lemieux,C.
Direct Submission
Submitted (24-MAR-1999) Biochimie, Universite Laval, Pavillon Charles Eugene Marchand, Quebec GIK 7P4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="M protein of photosystem II"
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                                            chloroplast genomes
Proc. Natl. Acad. Sci. U.S.A. 96 (18), 10248-10253 (1999)
99398694
                                                                                                                                                                                                                                                                                                                               /anticodon=(pos:1015, .1017, aa:Gln)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'anticodon=(pos:1136 .1138,aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /anticodon=(pos:1652. .1654,aa:Met)
                                                                                                                                                                                                                                1. .200799 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /anticodon=(pos:798. .800,aa:Leu)
                                                                                                                                                                                                                                                                       /organelle="plastid:chloroplast"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="ribosomal protein S14"
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332. .634
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                                                                                                                                                                                                             FEATURES
    TITLE
                                                                                                                                                              Schudy, A., Blechschmidt, K., Schillhabel, M., Baumgart, C., Menzel, U., Weber, J., Schattevoy, R. and Rosenthal, A.
Direct Submission
Submitted (06-JUL-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
Genome Sequencing Center Jena.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109723)
Schudy,A., Blechschmidt,K., Menzel,U., Polley,A., Reichwald,K., Rump,A., Schilnabel,M.B., Taudien,S., Wen,G., Schlegelberger,B., Siebert,R. and Rosenthal,A.

Chomosome 8 genomic sequence
                                                                                                                                                                                                                                                                                                                                   Submitted (24 MAN-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11. Jena 07745, Germany on Jun 1, 2000 this sequence version replaced gl:5514637.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
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Nephroselmis olivacea chloroplast DNA, complete genome.
AF137379
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Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
I (bases 1 to 200799)
Turmel, M., Otis, C. and Lemieux, C.
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/db_xref="taxon:9606"
/chromosome="8 map 8q12-8q13"
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/note="assembly_fragment
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/note="assembly_fragment
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complement 9442. 9846)
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RVYLTGGFKKPRELTWVTGVILAVITVSFGVTGYSLPWDQVGYMAVKIVTGVPDAIPV
IGAPLVELLRGSVSVGQSTLTRFYSLHTFVLPLLTAVFMLMHFLMIRKQGISGPL"
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The complete chloroplast DNA sequence of the green alga
Nephroselmis olivacea: insights into the architecture of ancestral
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Nephroselmis olivacea chloroplast DNA, complete genome.
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Pred. No. 77;
0; Mismatches
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/gene="rpl12"
complement(9045. .9431)
/gene="rpl12"
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/gene="rps9"
                                                                                                                                          .8779)
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LANSKTRKDQIENNLAFKRARVRYQVATLVK"
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DEWLYNGGCYELIVLHFLLGVACYNGREWELSFRLGMRPWIRVAYSARPVAATAVFLI
YPIGGSFSDGMPLGISGTRFMIVFORQAENULLMHPFHMLGVAGVFGGSLFSAMHGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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Direct Submission
Submitted (24-MAR-1999) Biochimie, Universite Laval, Pavillon
Charles-Eugene Marchand, Quebec GlK 7P4, Canada
Location/Qualifiers
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  TITLE
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us-09-380-826a-2.rge

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complement(9998. 11485)
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85.5%; Score 18.8; DB 6;
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Search completed: March 27, 2001, 08:17:03 Job time: 5900 sec

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jb_htg12:

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Minimum DB : Maximum DB :

Database

Searched:

OM nucleic

Run on:

Sequence:

Title:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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gb_htg23:

gb_sts2 qb_vi2: 19243 Leptospira 21634 Linadai ge 12674 Leptospira 12677 Leptospira 112670 Leptospira 112671 Leptospira 112671 Leptospira 221630 L.borgpeter 112673 Leptospira 221630 L.borgpeter 112673 Leptospira

WA4516S WA5216S LBU12670 LBU12669 LNU12671 LB16SRDNP

1513 1489 1516 1425 1486

1483 1489

LFA19243 LIRRN16S LI16SRDNY LFU60594

1481 1450

Length

U60594 Leptospira

Description

SUMMARIES

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gb_pat1:

gb_pat2:

L. interroga L. santarosa L. weilii ge L. noguchii

WB4616S LK46SRDNP LSU12672 LM16SRDNX L116SRN LZ116SRNN LW16SRDNY LN16SRDNP LLEPRR16SB LEPRR16SB LEPRR16SB LEPRR16SB LEPRR16SB

1410 1424 1523 1433

1419 1494 1418 1396 1415

Z21648 Z12817 Z21649 Z21637 Leptospira L.wolbachii

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Leptospira

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1022.2 69.2 1439 2 LBTM31994 298588 1003.6 67.9 1451 1 AAA16SRDNP 221629 1003.4 67.9 1321 2 LEPRR16SA M712A1 1003.4 67.9 136.6 1 AF167343 AF16734	995.8 67.7 144.2 LBTM31993 298.887 995.8 67.4 1410 2 CC16SRDNP 221631 993 67.2 1398 2 LB16SRRN 2126969 991 67.1 1394 2 LB16SRDN 226969	30 991.8 67.1 1394 2 LBTM21993 298592 Leptcospira 31 991.6 67.1 1527 2 LEPRRIGSC 221633 J. Jequitaia 32 991 67.1 1379 2 JJ16SRDNP 2208593 Leptcospira 33 985.8 66.7 1427 2 LBTM21994 298593 Leptcospira	977.8 66.2 1466 2 LEIMINISS 22163 972 65.8 1445 2 LIIGSRDNX 22163 964.4 65.3 1413 2 LEIM61994 25859 915.8 62.0 1543 29 UEAAJ9479 22697 00. 50 1265 27 UEASPINE	883.2 59.8 1475 29 UED81652 UEB8152 Unidentif 883.2 59.8 1494 2 PA16SRR X77216 P.acidigal 866.6 58.7 1494 2 CG16SRN X75272 Clostridium 866.6 58.7 1494 2 CG16SRN X75272 Clostridium 866.6 58.7 1454 2 CG16SRN X75272 Clostridium 866.6 58.7 1454 2 CG16SRN X75772 Malonmona X75772 Mal	860.70 28.7. 1522 CTIGSRNA 867.8 58.1 1532 1 AB039334 AB039 857.6 58.0 1379 2 LPIGSRDNP 22163	ALIGNMENTS	LFU60594 1481 bp	1100 1110000mat han 90007 Februar 11100	Leptospira falnei. Leptospira falnei. Bacteria: Spirochaetales; Leptospiraceae; Leptospira. Bacteria: Spirochaetales; Leptospiraceae; Leptospira.		MEDLINE 98404550 (REFERENCE 2 (bases 1 to 1481) AUTHORS Adler, B., Chappel, R.J., Baranton, G., Bulach, D.M., Billinghurst, M.L., Letocart, M., Merien, F., Serrano, M.S. and	TITLE Direct Submission JOURNAL Submitted (12-JUN-1996) Microbiology, Monash University, Wellington JOURNAL Rd., Clayton, VIC 3168, Australia Rd., Clayton, VIC 3168, Australia	rce	rRNA (11481) /product="16s ribosomal RNA" /product="16s ribosomal RNA" /product="16s ribosomal RNA" /product="16s ribosomal RNA" /product="16s ribosomal RNA"	watch 96.9%; Score 1431.4; DB 2; Length 1481;	0; Mismatches 1; Indels 4; Ga ggcggcgctcttaaacatgcaagtcgagcggggttag	DD 1 ĠATCATGGCTCAGAACTAACGCGGGGGGGCGTCTTAAACATGCAAGTCGAGCGGGGTAG bu Qy 61 caatacctagcggcgaacgggtgagtaacacgt-ggtaatcttcctccgagtctgggata 119

RESULT 1 LFU66594 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL MEDLINE REFERENCE AUTHORS

REFERENCE AUTHORS

BASE COUNT ORIGIN

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1 (bases 1 to 1450)
Petersen. A. M., Krogfelt, K. A., Perolat, P., Boye, K. and
Schlichting, P.
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0; Mismatches 9
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/strain="SSI 5402-98"
/db_xref="taxon:48782"
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/gene="16s rRNA"
/product="16s ribosomal + 1. .1450
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Krogfelt, K.A.
Direct Submission
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Submitted (22-NOV-1989) Fukunaga M., Faculty of Pharmacy and
Submitted (22-NOV-1989) Fukuyama University, 985 Higashimuracho,
Pharmaceutical Science, Fukuyama University, 985 Higashimuracho,
Pharmaceutical Science, Fukuyama University, 985 Higashimuracho,
2 (bases I to 1508)
Fukuyamashi, Hiroshimaken 729-0, Japan
Prukunaga, M., Horle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Horle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Gorle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Gorle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Horle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Horle, I., Okuzako, N. and Mituchi, I.
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Fukunaga, M., Horle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Horle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Horle, I., Okuzako, N. and Mituchi, I.
Fukunaga, M., Mituchi
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1. 1508
/organism="Leptospira interrogans"
/strain="serovar canicola strain Moulton"
//db_xref="taxon:173"
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165 ribosomal RNA; ribosomal RNA.
Leptospira interrogans.
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Bacteria; Spirochaetales;
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Fukunaga,M.
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
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Burnect Submission
Submitted Submission
Submitted, Delember 1993; Hookey J.V., Public Health Laboratory
Service, Leptospira Reference Laboratory, Stonebow Road, Hereford,
Herefordshire, United Kingdom, HRI 2ER
Location/Qualifiers
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Unpublished
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1 (bases 1 to 1374)
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2; Mismatches 4.
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/strain="LYME"
/db_xref="taxon:29506"
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Leptospira inadai
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Matches 1327; Conservative
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McClelland, M.
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                                                     Direct Submission
Submitted (25-JUL-1994) Michael McClelland, California Institute
Biological Research, 11099 North Torrey Pines Road, La Jolla, CA
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     Ralph,D. and McClelland,M.
Phylogenetic evidence for horizontal transfer of an intervening sequence between species in a spirochete genus
J. Bacteriol. 176 (19), 5982-5987 (1994)
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                                                                                            /organism="Leptospira weilii"
/strain="serogroup Celledoni, serovar
Celledoni (ATCC 43285)"
/isolate="NA45"
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Best Local Similarity 94.1%;
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McClelland, M.
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Ralph, D. and McClelland, M. Phylogenetic evidence for horizontal transfer of sequence between species in a spirochete genus J. Bacteriol. (1994) In press 2 (bases 1 to 1489)
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        and, California
Pines Road, La
                                          /organism="Leptospira weilli"
/strain="serogroup Hebdomadis, subserogroup
serovar worsfoldi, strain Worsfold"
/isolate="WA52"
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Direct Submission
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Biological Research, 11099
92037, USA
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Best Local Similarity 94.1%;
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Leptospira borgpetersenii Hardjo bovis/Sponselee 16S rRNA gene,
partial sequence.
U12670
U12670 GI:558929
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        ggggactatgctcgcaagagtgaactcaaaggaattgacggggtccgcacaagcggtg
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North Torrey Pines Road, La
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Leptospira borgpetersenii.
Bacteria: Spirochaetales; Leptospiraceae; Leptospira.
( pases 1 to 1513)
Ralph, D. and McClelland, M.
Phylogenetic evidence for horizontal transfer of an is sequence between species in a spirochete genus
2 (bases 1 to 1513)
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Submitted (25-JUL-1994) Mic
Biological Research, 11099
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/organism="Leptospira borg;
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/strain="serovar balcanica, strain 1627 Burgas"
/isolate="BD30"
/db_xref="taxon:174"
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Pines Road, La
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Leptospira borgpetersenii
Bacteria: Spirochaetales: Leptospiraceae; Leptospira
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Submitted (25-JUL-1994) Michael McClelland,
Biological Research, 11099 North Torrey Pine
92037, USA
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McClelland, M.
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North Torrey Pines Road, La Jolla, CA
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/strain="serogroup Autumnalis, subserogroup
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/isolate="NB36"
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Phylogenetic evidence for horizontal transfer c
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Submitted (25-JUL-1994) Michael
Biological Research, 11099 North
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                                                                                           DB 2; Length 1425
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L Submitted (09-FEB-1993) Hookey J.V., Public Health Lab Submitted (09-FEB-1993) Hookey J.V., Public Health Lab Service, Leptospira Reference Laboratory, Stonebow Roa Herefordshire, United Kingdom, HRI 2ER
Location/Qualifiers
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Astrain="Laboratory by Train" / Strain="Javanica VELDRAT BATAVIA 46" / db_xxef="taxon:174"
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ilarity 94.2%; Pred. No. 2.5e-13;
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Biological Research, 11099 North Torrey Pines Road, La Jolla, CA
92037, USA
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Ralph,D. and McClelland,M.
Phylogenetic evidence for horizontal transfer of sequence between species in a spirochete genus J. Bacteriol. 176 (19), 5982-5987 (1994)
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/db_xref="taxon:28184"
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McClelland, M.
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                                                                                                                                                                             Spirochaetes
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Submitted (09-FEB-1993) Hookey J.V., Public Health I
Service, Leptospira Reference Laboratory, Stonebow Herefordshire, United Kingdom, HR1 2ER
Location/Qualifiers
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                                                                                                                                                                                                                                                            /organism="Leptospira kirschneri"
/strain="CYNOPTERI 3522 C"
/db_xref="taxon:29507"
                                                                                                                                                                                                                                                                                                                                       Score 1246.6; DB 2;
Pred. No. 3.4e-13;
}; Mismatches 76;
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326 c 423 q 299 t
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16S ribosomal
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1 (bases 1 to 1419)
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Best Local Similarity 94.2%;
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                                                                                          LK16SRDNP 1419 bp
L.kirschneri gene for
Z21628
Z21628.1 GI:433582
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Leptospira kirschneri.
Leptospira kirschneri
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Institute Jolla, CA

nd, California Pines Road, La

(bases 1 to 1494)

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/strain="serogroup Tarassovi, subserogroup serovar atlantae, strain LT81" /isolate="SA39"

/db_xref="taxon:28183"

santarosai"

Location/Qualifiers 1. .1494 /organism="Leptospira

USA

an intervening

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Leptospira

Leptospira santarosai

GI:558931

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Phylogenetic evidence for horizontal transfer c
sequence between species in a spirochete genus
J. Bacteriol. 176 (19), 5982-5987 (1994)
                                                                                              Direct Submission
Submitted (25-JUL-1994) Michael McClelland,
Biological Research, 11099 North Torrey Pine
                                 Bacteria, Spirochaetales, Leptospiraceae,
1 (bases 1 to 1494)
Ralph, D. and McClelland, M.
                            Leptospira santarosai
                                                                   J. Bacteriol. 176
95014031
                                                                                        McClelland, M.
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 Length 1494;
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   DB 2;
 Score 1239.8; DB 2;
Pred. No. 4.1e-13;
0; Mismatches 92;
Query Match 83.9%;
Best Local Similarity 93.2%;
Matches 1363; Conservative
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BCT 18-FEB-1995 gene, partial sequence.

LSU12672 1494 bp DNA Leptospira santarosai LT81 16S rRNA

LOCUS

LSU12672

RESULT

Laboratory Road, Hereford,

Spirochaetes

related

to 1418)

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agctaataccggatagtcctgttggatcacaagatttgataggtaaagatttattgcttg 194
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Submitted (09-FEB-1993) Hookey J.V., Public Health I
Service, Leptospira Reference Laboratory, Stonebow I
Herefordshire, United Kingdom, HRI 2ER
Location/Qualifiers
                Phylogeny of Leptospiraceae and
                               (bases 1 to 1418)
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Matches 1337; Conserv
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                                      Hookey, J.V.
         Hookey, J.V.
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               taccagttgttgggggttttaacctcagtaacgaacctaacggattaagtagacgcct
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Length 1418;

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Score 1238.2; DB 2; Pred. No. 4.6e-13; 2; Mismatches 75;

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83.8%; llarity 94.2%; Conservative 2

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/product="16s ribosomal 324 c 421 q 29

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1. 1418 /organism="Leptospira r /strain="RANARUM ICF" /db_xref="taxon:29508"

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02-DEC-1993

(partial)

RNA

ribosomal DNA

LM16SRDNX 1418 bp L.meyeri gene for 16S 221648

LOCUS DEFINITION

LM16SRDNX

GI:433585

16S ribosomal RNA 221648.1

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

Leptospira meyeri. Leptospira meyeri Bacteria; Spirochaetales; Leptospiraceae; Leptospira

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Submitted (19-JUN-1992) Hookey J. V., Public Health Laboratory
Service, Leptospira Reference Laboratory, Stonebow Road, Hereford,
Herefordshire, United Kingdom, HRI 2ER
Location/Qualifiers
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1 (bases 1 to 1396)
1 tyden, J., Gatehouse, J.A. and Hookey, J.V.
Automated PCR cycle sequencing of 16S ribosomal RNA genes
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/strain="icterohaemorrhagiae RGA"
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Leptospira interrogans.
Leptospira interrogans
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L'interrogans 168 ribosomal RNA.
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                                                 Length 1396;
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                                                  DB 2;
                                                   , 6e-13;
72;
              ribosomal
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                                                Score 1232.8;
Pred. No. 5.6e-
0; Mismatches
      1. .1396
/standard_name="16S
319 c 418 g
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		į	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
0	7	100.0	10	81	AR062865	AR062865 Sequence
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ព	5 7	100.0	14	79	AX007734	AX007734 Sequence
o o	, 7	100.0	14	81	A25812	A25812 polynucleot
7	7	100.0	14	81	A40518	A40518 Sequence 55
ပ	7	100.0	14	81	A88271	A88271 Sequence 41
υ υ	7 7	100.0	14	81	A88273	A88273 Sequence 42
1.0	7	100.0	14	81	A89045	A89045 Sequence 11
c 11	7	100.0	14	81	A90238	A90238 Sequence 41
c 12	7	100.0	14	81	A90240	A90240 Sequence 42
c 13	7	100.0	14	81	126234	126234 Sequence 19
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c 15	5 7	100.0	15	81	A88272	A88272 Sequence 42
16	5 7	100.0	15	81	A88466	A88466 Sequence 61
c 17	7	100.0	15	81	A90239	A90239 Sequence 42
18	7	100.0	15	81	A90433	A90433 Sequence 61
15	7	100.0	15	81	AR033435	AR033435 Sequence
c 50	7	100.0	15	81	AR033480	AR033480 Sequence

157664 Sequence 20

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Stuyver, L. Method for detection of drug-selected mutations in the hiv protease \ensuremath{\mathsf{Method}}
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 14)
Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
A method for stimulating the immune system
Patent: WO 9963975-A 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
Location/Qualifiers
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    14 / Organism="Aids-associated retrovirus"

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hes 0;
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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Viruses; Retroid viruses; Retroviridae.
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0; Mismatches
PAPILLOMAVIRUS-INDUCED TUMOURS
Patent: WO 9010459-A 7 20-SEP-1990;
Transgene S.A
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Sequence 275 from Patent W09967428.
AX007733.1 GI:9995430
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Sequence 43 from Patent W09963975.
AX009010 GI:9996384
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/db_xref="taxon:9606"
3 c 4 g 4
                                                                        /organism="unidentified"
/db_xref="taxon:32644"
3 c 4 g
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A97828 Sequence 15
A97828 Sequence 10
AR084439 Sequence
I3444 Sequence
I52073 Sequence 32
I52073 Sequence 15
A65762 Sequence 43
A97904 Sequence 43
AR05555 Sequence
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113562 Sequence 4
115174 Sequence 23
132561 Sequence 25
137420 Sequence 43
150672 Sequence 4
153069 Sequence 81
189345 Sequence 81
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Patent: US 5843767-A 13 01-DEC-1998;
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A07301
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Nucleotide sequence 7 from patent number W09010459,
A00432
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iive 0; Mismatches
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Sequence 13 from patent US 5843767.
AR062865 GI:5990556
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AR053055
AR053056
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AR093881
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A45212
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Beattie, K.L.
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Best Local Similarity 100.
Matches 7; Conservative
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REFERENCE AUTHORS TITLE

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ANTISENSE-OLIGONUCLECTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b)) Patent: WO 9425578-A 55 10-NOV-1994; BIOGNOSTIK GES (DE)
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AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Sequence 419 from Patent WO9833904.
A88271
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Sequence 55 from Patent W09425578.
A40518
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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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/organism="Aids-associated retrovirus"
/db_xref="taxon:11966"
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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4 c 2 g 4 t
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Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
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Sequence 276 from Patent W09967428.
AX007734
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/db_xref="taxon:11966"
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polynucleotide 14C12.
A25812
A25812.1 GI:904780
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artificial sequence.
1 (bases 1 to 14)
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Stuyver, L.
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Best Local Similarity
Matches 7; Conserv
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ACCESSION VERSION KEYWORDS SOURCE

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1 (bases 1 to 14)
Vergnand, G.
Process for detection of new polymorphic loci in a DNA sequence, nucleotide sequences forming hybridization probes and their
                                                                                                                                                                             100.0%; Score 7; DB 81; Length 14; 100.0%; Pred. No. 5e+05; Live 0; Mismatches 0; Indels
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Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonuclectide preparation method
Patent: EP (0856579-A 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
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Patent: US 5556955-A 19 17-SEP-1996;
Location/Qualifiers
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Sequence 19 from patent US 5556955.
126234
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Sequence 421 from Patent EP0856579.
A90240
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     Patent: EP 0856579-A 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
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1 (bases 1 to 14)

Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

PATENTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

PATENTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

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LOCALION/QUALIFIERS
                                                                                                        1 (bases 1 to 14)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD PATENT: WO 9833904-A 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
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Sequence 1193 from Patent WO9833904.
AB9045.
AB9045.1 GI:6737615
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Sequence 419 from Patent EP0856579.
A90238.1 GI:6738752
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A88273
A88273.1 GI:6736843
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AUTHORS TITLE JOURNAL

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RESULT 11 A90238/c LOCUS DEFINITION

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ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

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Aids-associated retrovirus.
Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
1 (bases 1 to 15)
Stuyver,L.
Method for detection of drug-selected mutations in the hiv protease
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unidentified
unclassified.
1 (bases 1 to 15)
Brysch,W. and Schlingensiepen,K.
AN ANTISENSE OLICONUCLECTIDE PREPARATION METHOD
Patent: WO 9833904-A 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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/organism="Aids-associated retrovirus"
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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Sequence 274 from Patent WO9967428.
AX007732
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Sequence 420 from Patent W09833904.
A88272
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/organism="unidentified"
/db_xref="taxon:32644"
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Search completed: March 27, 2001, 08:17:04 Job time: 5901 sec

Integrin alpha 6 s Human C-raf target HIV-1 protease gen HIV-1 protease gen Immunosuppressant Substrate for hair Sequence of initia Human CD40 hammerh Mouse B7-2 hammerh Human B7-2 hammerh Human B7-2 hammerh Rabbit CETP HH rib Rabbit CETP HH rib Rabbit CETP HH rib Rabbit CETP HH sib Fragene antisense Erba-2 gene antisense Erba-2 gene antisense Erba-2 gene pro-Human NR8 gene pro-

7 100.0 14 20 7 100.0 14 20 7 100.0 14 21 7 100.0 14 21	17 7 100.0 14 21 265483 18 7 100.0 14 21 264788 19 7 100.0 15 2 N10044	20 7 100.0 15 2 N10045 21 7 100.0 15 17 X66445 22 7 100.0 15 17 X66275	7 100.0 15 17 7 100.0 15 17 7 100.0 15 17	26 7 100.0 15 17 x66236 27 7 100.0 15 17 x66237	28 7 100.0 15 17 X66238 29 7 100.0 15 17 X65872	30 7 100.0 15 17 X65873 31 7 100.0 15 17 T50248	32 7 100.0 15 17 T50250 33 7 100.0 15 19 V49025	7 100.0 15 19 V48831 EPE 7 100.0 15 20 X31673 Tag 7 100.0 15 21 259285 Hung	7 100.0 15 21 259298 7 100.0 15 21 259299 7 100.0 15 21 290823 7 100.0 15 21 290839	100.0 15 21 290896 Hum 100.0 15 21 290805 Hum 100.0 15 21 2597784 HIV 100.0 15 21 262590 Sub 100.0 15 21 262639 Sub	ALIGNMENTS	RESULT 1	3898 V588	XX AC V58998;	XX DT 20-JAN-1999 (first entry)	DE Leptospira nucleotide sequence.	<pre>AA KW Infection; pathogenic Leptospira; protective immunity; therapy; KW diagnosis; ss. vy</pre>	OS Leptospira sp. XX XX W09840099-A1.	PD 17-SEP-1998.	XX	AA PR 07-MAR-1997; 97AU-0005494.	PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD. PA (PIGR-) PIG RES 6 DEV CORP.	AA PI Chappel RJ;	DR WPI; 1998-520791/44.	PT New isolated pathogenic Leptospira bacterium - useful for, e PT developing products for conferring protective immunity, and i PT prophylactic or therapeutic treatment
4.5 Compugen Ltd.		earch time 207.51 Seconds (without alignments) 12.672 Million cell updates/sec					: 960044	,		eqn/NA1980.DAT:* eqn/NA1981.DAT:* eqn/NA1982.DAT:*	eqn/NA1983.DAT:* eqn/NA1984.DAT:* eqn/NA1985.DAT:*	eqn/NA1987.DAT:* eqn/NA1988.DAT:*	DAT	DAT	DAT	sequ/NA1996.DA1:*	DAT	,	3		Description	Leptospira nucleot Human parkin gene	numan denortito ce Metastatic breast Metastatic breast	Metastatic breast N11 active EGS 22	Hypervariable regi Antisense oligonuc Potato citrate syn
GenCore version 4.5 Copyright (c) 1993 - 2000 Comp	earch, using sw model	March 27, 2001, 08:22:58 ; Search (With	-0860-s	1 tgttgga 7	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	480022 seqs, 187831343 residues	hits satisfying chosen parameters	length: 0 Length: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Geneseq_36: /cgn2_2/gc /cgn2_2/gc /cgn2_2/gc	 4: /cgn2_1/gcgdata/geneseq/genes 5: /cgn2_2/gcgdata/geneseq/genes 6: /cgn2_2/gcgdata/geneseq/genes 7: /cqn2_2/gcgdata/geneseq/genes 	8: /cgn2_2/gcgdata/geneseq/genes 9: /cgn2_2/gcgdata/geneseq/genes	10: /cgn2_2/gcgdata/geneseg/gene	12: /cgn2_2/gcgdata/geneseq/gene 13: /cgn2_2/gcgdata/geneseq/gene	14: /cgnz_z/gcgdata/geneseq/gene 15: /cgnz_z/gcgdata/geneseq/gene 16: /cgnz_z/gcgdata/geneseq/gene	17: /cgn2_1/gcgdata/geneseq/gene 17: /cgn2_1/gcgdata/geneseq/gene 18: /cgn2_1/gcgdata/geneseq/gene	19: /cgn2_2/gcgdata/genesequ/genesequ/NAL9 20: /cgn2_2/gcgdata/geneseq/geneseqn/NAL9 20: /cgn2_2/gcgdata/geneseq/geneseqn/NAL9 21: /cgn2_2/gcgdata/geneseq/geneseqn/NAL9	the number of results predition or equal to the score	לייים ביים ביים ביים	SUMMARIES	Match Length DB ID	10 20	10 21	.0 10 21	100.0 14 14 040606 100.0 14 15 078406 100.0 14 19 v97198
	nucleic -	Run on:	Title: Perfect score:	(1)	Scoring table:	Searched:	Total number of	Minimum DB seq 1. Maximum DB seq 1.	Post-processing:	Database :								Pred. No. score grea	1	Result	Score			6 7	c 8 7 7 c 10 7

Human dendritic cell SAGE tag, SEQ ID NO:679.

(first entry)

10-APR-2000

278251;

BP.

Z78251 standard; DNA; 10

RESULT Z78251

9 TGTTGGA 3

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             This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a fragment of an intron from the gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkinson's disease related gene; parkin gene; variant; gene therapy;
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100.0%; Pred. No. 5.2e+07;
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                                                                                                                    diagnosis of past or present LS infection.
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(SHIM/) SHIMIZU N.
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Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer \cdot
                                                         SAGE tag: serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                           cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences 277573-279709 represent SAGE (serial analysis of gene expression) tagg used to identify mWNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 84; 130pp; English.
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98US-0090039.
98US-0090040.
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98US-0090042.
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98US-0090045.
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(ROBE/)
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0;

Gaps

; 0

100.0%; Score 7; DB 20; Length 10; 100.0%; Pred. No. 1.4e+04; Live 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 7; Conservative

Query Match

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complexy and subsequent recognition by Treal receptors is alone
insufficient to activate a robust cytotoxic immune response that can lyse
the tumour cells, immunostimulatory cofactors also being required for
the tumour cells, immunostimulatory cofactors also being required for
cefficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic caid
sequences identified using the SAGE tags have several potential uses.
They may be used in vaccines to induce an immune response, particularly
against a tumour antigen; to modulate the genotype of an APC; to screen
for agents that modulate expression of differentially expressed genes in
an APC; and as hybridisation probes/amplification primers for the
capression of these genes. Detection of the dendritic cell differentially
expressed genes, or of their encoded proteins, can be used to identify
cells as belonging to the monocyte lineage. Cells containing these genes
can be used in active immunotherapy (or to stimulate production of a
population of antigen-specific effector cells) and vectors containing
APC-associated costimulatory factors ensures adequate antigen
are used in gene therapy. Co-administration of tumour antigens and
APC-associated costimulatory factors ensures adequate antigen
bresentation of or costimulatory signals, migration to Tcell-rich sites,
secretion of Tcell growth factors and secretion of chemokines for
recruitment of immune effector cells.
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                                                          other transcripts correspond to novel genes. Antigen-presenting cell APO, associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MMC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone
with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while
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Matches 7; Conservative 0;
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98US-0089997.
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ROBERTS B L.
SHANKARA S.
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19-JUN-1998;
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Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antisen-encoding sequence for use in gene or cell-based vaccines; Polypeptides encoded by the transcripts are also useful in vaccines; for diagnoship breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antisen specific immune effecter cells, c.g. cytotoxic T lymphocytes, and these used for adoptive
                                                                                                                                                                                                                                                                                                                                                                        that are preferentially transcribed in the metastatic breast tumour 153sue (i.e. are upregulated in metastatic breast tumour cells). 283942 to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.
                                                                                                                                                                                                                                                                                                                                         280767 to 283941 represent tags corresponding to distinct transcripts
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                                                                                                                                 Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
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100.0%; Pred. No. 1.4e+04;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                          Claim 1; Page 63; 219pp; English.
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98US-0090041.
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       Shankara S;
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Best Local Similarity
Tr Conserve
                                                                  WPI; 2000-106079/09.
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Roberts BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1999.
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98US-0090041

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19-JUN-1998;
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that are preferentially transcribed in the metastatic breast tumour cells. 283941 represent tags corresponding to distinct transcribts that are preferentially transcribed in metastatic breast tumour cells). 283942 to 286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic biggnosis is by standard immunoasays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based cancernes Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic genes; cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter colls.
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                                                                                   Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metastatic breast tumour cell downregulated transcript tag #3531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 7; DB 21; 1
100.0%; Pred. No. 1.4e+04;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 2 A; 0 C; 4 G; 4 T; 0 other;
                                                                                                                                         Claim 1; Page 110; 219pp; English.
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98US-0090039.
98US-0090040.
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Best Local Similarity 100.
Matches 7; Conservative
                                       Shankara S;
   (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.
                                                              WPI; 2000-106079/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                  immunotherapy.
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19-JUN-1998;
19-JUN-1998;
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                                        Roberts BL,
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that are preferentially transcribed in the metastatic breast tumour cells.

that are preferentially transcribed in the metastatic breast tumour cells.

that are preferentially transcribed in metastatic breast tumour cells). 283942

to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic biagnosis is compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).

compounds that an antigen-encoding sequence for use in gene or cell-based particularly an antigen-encoding sequence for use in gene or cell-based cancines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            target mRNA; identification; diagnostic;
therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                   Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis,
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Pred. No. 1.4e+04;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10 BP; 2 A; 0 C; 3 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                     prevention and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 153; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0079851.
97US-0976220.
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ID X77658 standard; DNA; 11 BP.
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                                                                                                                             Shankara
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Best Local Similarity
7; Conserva
(GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                                                        WPI; 2000-106079/09
                                                                 SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N11 active EGS 22
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||||||||
2 tgttgga 8
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21-NOV-1997;
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                                                                                                                             Roberts BL,
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                                                                                                                                                                  This invention describes a novel method allowing essential or functional genes to be rapidly identified and inactivated. The method is able to firstly identify most of the essential genes in an organism (1.e. a bacteria or a eukaryote) needed for survival, and secondly it provides for reducing or inactivating their expression. The method is able to diagnostic reagents and therapeutics. The method provides a means for identify functional oligoniclectide molecules able to be used as diagnostic reagents and therapeutics. The method provides a means for identifying essential genes whose sequence is known only as part of a genome with unknown function, as well as a means for identifying concluded to morprising (a) a first reporter gene encoding a nucleic acid molecule comprising (a) a first reporter gene encoding a functional oligonucleotide molecule such as an external guide sequence concoting a second reporter protein, and (c) a targeting gene encoding a encoding a second reporter protein, and (c) a targeting gene encoding a functional oligonucleotide molecule such as an external guide sequence (EGS), a ribozyme or an antisense RNA and targeted to the RNA of interest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVR; human; animal; forensic science; paternity testing; diagnosis; animal breeding; hereditary diseases; tumours; allele; loss; chromosomal regions; tumour region identification; ss.
                                                                                                Identifying and inhibiting functional nucleic acid molecules in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; DB 20; Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypervariable region detection probe 14C12.
                                          Robertson HD;
                                                                                                                                             Example 3; Page 28; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
             (INNO-) INNOVIR LAB INC.
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                                         Nilsen TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-136548/17.
                                                                     WPI; 1999-357853/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
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                                         Kindt TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              040606;
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Detecting the hypervariable regions of DNA for diagnosing

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Gaps
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                                                                                                                      The sequence is that of a polynucleotide probe which may be used in the detection of new hypervariable regions (HVR) in a DNA sequence. HVR represent a fingerprint useful in e.g. forensic science, paternity testing, animal breading, etc. The probe may be used as part of a method for the efficient detection in humans or other animals, without the use of mini-satellites or primary enrichment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour; angiogenesis; breast tumour; neurofibroma; giloma; glioblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut; immunosuppression; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth factor beta; TGF-beta; antisense; treatment;
                                                                                                                                                                                                                                                                                                                                                                                 ö
hereditary illnesses and tumours - by hybridising labelled polynucleotides and analysing genomic DNA of individuals which react with restriction fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating immunosuppression, tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlingensiepen G, Schlingensiepen
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 7; DB 14; Length 14; 100.0%; Pred. No. 1.4e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense oligonucleotide hybridising to TGF-beta gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transforming growth factor beta anti:sense oligo:nucleotide(s) - for treating immunosuppy
                                                                                                                                                                                                                                                                        Sequence 14 BP; 4 A; 4 C; 2 G; 4 T; 0 other;
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                                                                                 Example; Page 13; 46pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q78406 standard; DNA; 14 BP
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93EP-0107849
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Schlingensiepen R;
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TGTTGGA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  078406;
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5555×8
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                                                                                                                                                          ó
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid biosynthesis or regulating flowering
See Q78352-Q78408. The sequences given in GENESEQ files Q78352-Q78407 and Q78488 are antisense oligodeoxynucleotides of TGF-beta 1. The sequences given in GENESEQ files Q78408-78487 are antisense oligodeoxynucleotides of TGF-beta 2 in the form of
                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                       Solanidine; glucosyltransferase; potato; citrate synthase; ta
hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
flower formation; cleavage; solanaceous plant; ss.
                                                                                                                             100.0%; Score 7; DB 15; Length 14; 100.0%; Pred. No. 1.4e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Potato citrate synthase target sequence position 123.
                                                                                       Sequence 14 BP; 3 A; 3 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 54; Page 59; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0979416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0036545.
                                                                                                                                                                                                                                                                    RESULT 10
V97198/c
ID V97198 standard; RNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US00738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                        01-MAR-1999 (first entry)
                                                              phosphorothioate analogues
                                                                                                                          Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zwick MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-427939/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum.
                                                                                                                                                                                             1 tgttgga 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McSwiggen JA,
                                                                                                                                                                                                                         3 tgttgga 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1997;
28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9832843-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-1998
                                                                                                                                                                                                                                                                                                                            V97198;
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ExbB-2 gene. Of these, only oligonucleotides directed against the ExbB-2 gene. Of these, only oligonucleotides V48709-91 resulted in significant redcution in ExbB-2 protein expression, while oligonucleotides V48702-886 had little effect. The oligonucleotides V48702-886 had little effect. The oligonucleotides can each form three hydrogen bonds to cytosines a nucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides ach able to form three H-bonds contain four cytosines, and the ratio between residues able to form two H-bonds each cytosines, and the ratio between residues able to form two H-bonds each cytosines, and the ratio between residues able to form two H-bonds each oligonucleotides are used to modulate expression of genes, particularly the genes for p53 ErB-2, junb, igno, 787 beta 1 or beta 2 to control conferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoblasts and/or kertainocytes). The coligonucleotides can also be used to analyse function of proteins (by a control the dense to the control of primary cell cultures (e.g. bone marrow stem, liver or altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate
ribozymes can be targeted to specific genes or to consensus sequences within a family of related genes, and being catalytic need to be present at only very low concentrations.
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ErbB-2; antisense oligonucleotide; modulate; gene expression; ss
                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                  Length 14;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ErbB-2 gene antisense oligonucleotide ErbB-2-N-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                        Mismatches 0:
                                                                                                                                                                                                                                              100.0%; Score 7; DB 19;
ilarity 100.0%; Pred. No. 1.4e+04
Conservative 0; Mismatches 0
                                                                                                                                                    4 A; 4 C; 5 G; 1 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlingensiepen K;
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                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                               Sequence 14 BP;
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13 TGTTGGA 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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V48830/c
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Pred. No. 1.4e+04;

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A21661
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                                                                                                                                                                                                            ExpB-2 gene. Of these, only oligonucleotides utages used a significant redcution in ExbB-2 protein expression, while coligonucleotides was a significant redcution in ExbB-2 protein expression, while coligonucleotides where the oligonucleotides can exemplify the invention. The specification describes oligonucleotides can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cutive cytosines; do not contain two sequences of three consecutive cutive cytosines; and the ratio between residues able to form two H-bonds each cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The cytosines, and the ratio between residues able to form two H-bonds each coliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoblasts and/or keratinocytes). The control of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoblasts, osteoblasts and/or keratinocytes). The coligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of concer or (targeting TGF) for stimulating the immune system.
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                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V48709-886 represent antisense oligonucleotides directed against the
                                                                                                                                                                                                                                                                                                                                                                                                              ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.
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0
                                                        Length 14;
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                           ErbB-2 gene antisense oligonucleotide ErbB-2-N-41.
                                                      DB 19; L
1.4e+04;
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Sequence 14 BP; 5 A; 4 C; 0 G; 5 T; 0 other;
                                                                                            Mismatches
                                                      Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 6c; 286pp; English.
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                                                      100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                               1 tgttgga 7
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11 TGTTGGA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-1997;
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                                                                                                                                                                                                                                                                                                    V48832;
                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                               V48832/c
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Score 7; DB 19; Length 14;

100.08;

Query Match

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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin alpha 6 subunit gene, and A1762 represent ribozyme sequences; A1768 and A19087 to A19154 represent crorresponding target sequences; A1768 and A19087 to A19155 to A19122 cropresent their corresponding target sequences; A1769 and A19087 to A19155 to A19122 cropresent ribozyme sequences; A1569 to A2150 and A21595 represent ribozyme sequences; A1689 to A2150 to A2159 to A2340 to A2150 and A21596 to A21608 represent their corresponding target sequences; A1689 to A2475 and A23476 to A2350, A2343 to A2343 to A2342 represent their corresponding target sequences for integrin subunit beta 3, and A2476 to A2352, A2343 to A2342 represent their corresponding target sequences. A1689 to A2475 and A23476 to A2352, A2343 to A2342 represent their corresponding target sequences. A1689 to A2475 and A2346 to A2352, A23343 to A2342 represent their corresponding target sequences. A1689 to A2475 and A2346 to A2352, A23343 to A2343 to A2340 to A2352, A2343 to A2340 to A2362, A2362, A2343 to A2362, A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; anglogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; anglogenic factor; cytostatic; antidabetic; ophthalmologic; antidniflammatory; antiarthitic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; veruca vulgaris; anglofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an anglogenic factors
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                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin alpha 6 subunit target site SEQ ID NO:4887.
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                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jarvis T,
100.08; PAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A21661 standard; RNA; 14 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2000 (first entry)
                                                                                      7; Conservative
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                                 Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                             1 tgttgga 7
                                                                                                                                                                                                                                  12 TGTTGGA 6
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                                                                                                ;
0
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation: expression: Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphospheres used as antiviral agents and synthons
                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beigelman L, Bellon L, Burgin A, Jarvis T;
A, Kisich K, Matulic-Adamic J, McSwiggen JA;
Reynolds M, Sweedler D, Thompson J, Workman CT;
                                                               Length 14;
                                                                    Score ', _____ Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                     Human C-raf target sequence nucleotide position 1952.
                                                                 Score 7; DB 20;
               5 A; 1 C; 4 G; 4 U; 0 other;
                                                                                                  3; Mismatches
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                                                                  100.08;
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97US-0049002.
97US-0051718.
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97US-0061321.
97US-0061324.
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ID V92044 standard; RNA; 14 BP.
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                                                                                    57.1%;
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09-JUN-1997;
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                   Sequence 14
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mutations in diseased cells and to determine c-raf RNA. Specifically NACS with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. V90922 to V93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene.
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                                                                                                                                                                                                                                                                                         Sequence 14 BP; 4 A; 5 C; 3 G; 2 U; 0 other;
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Pred. No. 1.46
; Mismatches
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Matches 7; Conservative 0; Mismatches 0; Indels

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1 tgttgga 7 ||||||| 12 TGTTGGA 6 ò g

Search completed: March 27, 2001, 08:22:59 Job time: 5301 sec

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Run on:

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U94974 Leptospira
U94975 Leptospira
U94976 Leptospira
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U60594 Leptospira AB007014 Spirochae AF003953 Leptospir

Description

us-09-380-826a-7.rge

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/db_xref="taxon:173"
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                                    GI:2516255
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Query Match
Best Local Similarity 95.5%
Matches 21; Conservative
                                                         Spirochaeta sp. (su
strain:FO-95) DNA.
                                                16S ribosomal RNA.
                                                                     strain:FO-95)
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Direct Submission
Submitted (12-JUN-1996) Microbiology, Monash University, Wellington Submitted (12-JUN-1996) Australia
Rd., Clayton, VIC 3168, Australia
Location/Qualifiers
                                                                                   ACO21155 Home sapt
ACO2155 Home sapt
AF77572 Unculture
AF01857 Unidentif
D49367 Lithospermu
273136 S.cerevisia
U40812 Stronghloce
U41016 Caenorhabdi
U41545 Caenorhabdi
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AC083790 Homo sapi
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AC003114 Arabidops
AB008265 Arabidops
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AL078470 Arabidops
Z98052 Human DNA
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ACO26320 Homo sapi
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(pases 1 to 1481)
Perolat, P., Chappel, R.J., Adler, B., Baranton, G., Bulach, D.M., Billinghurst, M.L., Letocart, M., Merien, F. and Serrano, M.S. Leptospira fainel sp. nov., isolated from pigs in Australia Int. J. Syst. Bacteriol. 48 Pt. 3, 851-858 (1998)
                                                                                                                                                                                                                                                                                                                     LFUG0594 1481 bp DNA BCT 10-SEP-1998
Leptospira fainei 16S ribosomal RNA gene, partial sequence.
UG0594
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Adler, B., Chappel, R.J., Baranton, G., Bulach, D.M.,
Billinghurst, M.L., Letocart, M., Merien, F., Serrano, M.S. and
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/strain="Hurstbridge"
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CELC02F12
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Schröchaeta Sp.
Bacteria: Spirochaetales; Spirochaetaceae; Spirochaeta.
Bacteria: Spirochaetales; Spirochaetaceae; Spirochaeta.
Bacteria: Spirochaetales; Spirochaetaceae; Spirochaeta.
El (bases 1 to 354)
Shin, M.-Se.
Direct Submission
AL Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun ALDOCATORY OF Marine Molecular Microbiology, Faculty of Shin, Laboratory of Marine Molecular Microbiology, Faculty of Shin, Laboratory of Marine Molecular Microbiology, Faculty of Shin, Laboratory 10, 306-01, Japan (E-mail:misun@kais.kyoto-u.ac.jp, 7-1075-753-6224, Fax:075-753-6226)
CE 2 (sites)
Tel:075-753-6224, Fax:075-753-6226)
CE 2 (sites)
From M. Yoshinaga. I., Uchida, A. and Ishida, Y.
Bylogenetic analysis by 165 rRNA gene sequencing of Obligate Oligotrophis isolated from the northern basin of Lake Biwa (Mesotrophic Lake)
Chigotrophic Lake)
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Leptospira interrogans strain 48/95 16S ribosomal RNA gene, partial
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Leptospira interrogans
Bacteria: Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 283)
Woo,T.H.S., Patel,B.K.C., Cinco,M., Smythe,L.D., Symonds,M.,
Norris,M. and Dohnt,M.
Norris,M. and Dohnt,M.
Identification of Leptonema by real-time homogeneous assay of incycle PCR product
Unpublished
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Spirochaeta sp. 16S rRNA gene, partial sequence.
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/organism="Leptospira interrogans"
/strain="48/95"
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                                                                                                                                                                                                                                                                                                                Bacteria; Spirochaetales; Leptospiraceae; Leptospira.

1 (bases 1 to 288)

Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,

Brenner,D.J. and Patel,B.K.C.

Identification of Leptospira inadai by continuously monitoring fluorescence during rapid cycle PCR
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.

(Dases 1 to 288)

Woo,T.H.S. Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,

Brenner,D.J. and Patel,B.K.C.

Identification of Leptospira inadai by continuously monitoring

Unpublished
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Leptospira inadai 16S ribosomal RNA gene, partial sequence
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Leptospira inadai 16S ribosomal RNA gene, partial sequence.
U94974
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 280)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.G. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Leptospira inadai 16S ribosomal RNA gene, partial sequence.
U94977
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Leptospira inadai 165 ribosomal RNA gene, partial sequence.
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Woo_T.H.S., Smythe.L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MAR-1997) School of Science, Griffith Unive
2 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M., Wroo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M., Brenner,D.J. and Patel,B.K.C.
Direct Submission
Direct Submission Patel,B.K.C.
Submitted (24-MAR-1997) School of Science, Griffith Unive Brisbane, QLD 4111, Australia
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/db_xref="taxon:29506
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Best Local Similarity 90.9
Matches 20; Conservative
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JOURNAL REFERENCE AUTHORS sontce

FEATURES

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Direct Submission Submission Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Safur, Laboratory of Marine Molecular Microbiology, Faculty of Agriculture, Kyoto University; Oiwakecho, Kitashirakawa, Sakyoku, Kyoto, 306-01, Japan (E-mail:misun@kais.kyoto-u.ac.jp, Tel:075-753-6224, Fax:075-753-6226)
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MR-1997) School of Science, Griffith University,
Brisbane, QLD 4111, Australia
Location/Qualifiers
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Shin, Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishida, Y.
Phylogenetic analysis by 16S rRNA gene sequencing of Obligate
Phylogenetic analysis by 16S rRNA gene sequencing of Obligate
Oliqotrophis isolated from the northern basin of Lake Biwa
(Mesotrophic Lake)
                                                                                                                                                                                                                                                                       Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
                                                                                                                   LIU94979 288 bp DNA BCT 01-JAN-1998
Leptospira inadai 16s ribosomal RNA gene, partial sequence.
U94979
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Spirochaeta sp. (sub_species:Freshwater obligate oligotroph,
strain:SO-104) DNA.
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Bacteria; Spirochaetales; Spirochaetaceae; Spirochaeta.
1 (bases 1 to 353)
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Spirochaeta sp. 16S rRNA gene, partial sequence.
AB007012
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Pred. No. 1.4e+02;
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61 c 88 g 6
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/db_xref="taxon:29506"
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90.9%;
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Bacteria; Splirochaetales; Leptospiraceae; Leptospira.
Bacteria; Splirochaetales; Symonds,M., Norris,M., Dohnt,M.,
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Bronner,D.J., and Patell,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
                                                                                                                                                                                                             2 (bases 1 to 288)

Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,

Brenner,D.J. and Patel,B.K.C.

Direct Submission

Submitted (24-MAR-1997) School of Science, Griffith University,

Brisbane, QLD 4111, Australia
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Leptospira inadai 165 ribosomal RNA gene, partial sequence.
U94978
U94978.1 GI:2735450
                                                                  Bacteria: Spirochaetales; Leptospiraceae; Leptospira.

(bases 1 to 288)

Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel.B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Woo.T.H.S., Smythe.L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MAR-1997) School of Science, Griffith Universibane, QLD 4111, Australia
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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/strain="218/95"
/db_xref="taxon:29506"
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/strain="268/95"
/db_xref="taxon:29506"
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61 c 88 g
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1012)
Taylor,C.B., Bariola, P.A., delCardayre,S.B., Raines,R.T. and
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/db_xref="GI:289210"
/translation="MASRLCLLLLVACIAGAFAGDVIELNRSQREFDYFALSLQWPGT
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IEKYWPSLGSGSPSSGNGGKGSFWGHEWEKHGTCSSPVFHDEYNYFLTLNLYLKHNY
TDVLYQAGYVASNSEKYPLGGIVTALQNAFHITPEVVCKRDAIDEIRICFYKDFKPRD
CVGSQDLTSRKSCYSLPEVTPLGEAMVLKMPTEREAL"

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RNS2: a senescence-associated RNase of Arabidopsis that diverged
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Arabidopsis thaliana ribonuclease (RNS2) mRNA, complete cds.
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Proc. Natl. Acad. Sci. U.S.A. 90 (11), 5118-5122 (1993)
93281708
      85.5%; Score 18.8; DB 7; Length 1012; 90.9%; Pred. No. 1.3e+02; ive 0; Mismatches 2; Indels 0
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    7organism="Arabidopsis thaliana"
/db_raf="taxon:3702"
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/gene="At2g39740"
/note="T517.4; predicted by genscan"
join(18783. 1891.19188. .19352,19496. .19674,19766. .19861,
1965. .20034,20131. .20261,20593. .21237)
/gene="At2g39740"
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/note="alternative splice form 2 GP|166835|M86720"
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/product="nubsico activase"
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IGINGSGGGGRSGCGENGARMGNGINPHWARGELSGNAGELSGRAGERSKLIRGYRREADLIK
                                                                                        KGKMCCLFINDLDAGAGRMGGTTQYTVNNQMYNATLMNIADNPTNVQLPGMYNKEENA
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CTDPVAENFDPTARSDDGTCXTVF
AQSNKKSNGSFKVLAVKEDKQTDGDEWRGLAYDTSDDQQDITRGKGMVDSVFQAPMGT
GTHHAVLSSYEYVSQGLRQYNLDNMMDGFYIAPAFMDKLVVHITKNFLTLPNIKVPLI
LGINGGKGQGKSFQCELVMAKMGINEIMMSAGELESGNAGEPAKLIRORYREAADLIK
                                                                                                                                                                                                                                         complement(join(13579, .13599,13713, .14005,14007, .14559,
14651, .14736,14836, .14941,15033, .15349,15834, .15878))
/gene="At2g39730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF165146 109723 bp DNA HTG 01-JUN-2000 Homo sapiens chromosome 8 map 8q12-8q13 clone CTA-397H3, WORKING DRAFT SEQUENCE, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .>24814)
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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90.9%;
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Best Local Similarity
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AF165146.
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KEYWORDS
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dgne="Artg39730"

/note="T517.3"

13364. .13461

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SDSSGFLLLGDAKSYMLGPTQTFLLOSTPLPYFDRVATTVQLEGITVGSKTSKTSCJS
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DLCYKVGSTTRPNFSGLPMVSLMFRGPYTALKFTTQTKSVLRLVDDPDFVFGGTM
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SDLLGTEAFYIGHHPQNYWMEDDLAKSRVGFAGNVRCDLASQRLGLRD"
COMPLONENT (< 1003) . 11304)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHHIYHPDCILPWLAIRNSCPVCRHELPAEDLTDGTGAALTAVTATAEEEEDSAAGLT
IWRLPGGGFAVGRIPGGWRGGDRMMPVVYTEVDGGRLGDERLPRRVAWGSRRGGRDGG
GSRERGGGFAGRIMRLFGCFSGSSGSIAAAAAASSGSGSRIRVTRRTRSFSMFSTASS
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typt_family="POLY_A"

complement(join(1323. .13599,13724. .14005,14087. .14559,

14651. .14736,14836. .14941,15033. .15349,15834. .16055))

/gene="At2g39730"
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14651. 14736,14836. 14941,15033. 15349,15834. 16055))
/gene="At2g39730"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"TSI7.1; similar to
pp. [2245.012 gnl.]prD[e327000]297341"
complement(4584. 5909)
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                                                                                                                            T517"
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complement(2759. .2862)
/rpt_family="poly_A"
complement(4584. .>5909)
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/gene="At2g39720"
                                                                                                                            /note="Sequence from clone
complement(130, 198)
/rpt_family="(CAAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="unknown protein"/codon_start=1
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complement(1266..1291)
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CDS

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HQLODLPVNSVPCRLHNRCTITGRPKGYYRDFGLSRHELRAMAHGCLLPGVTKASW"
            The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral
                                                                                                                                                              Turmel, M., Otis,C. and Lemieux,C.
Direct Submission
L Submitted (24-MAR-1999) Biochimie, Universite Laval, Pavillon
Charles-Eugene Marchand, Quebec GlK 7P4, Canada
Location/Qualifiers
rce
//organism="Nephroselmis Olivacea"
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//organism="Nephroselmis Olivacea"
//organism="Nephroselmis Olivacea"
//organism="Nephroselmis Olivacea"
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                                                                   chioroplast genomes
Proc. Natl. Acad. Sci. U.S.A. 96 (18), 10248-10253 (1999)
99398694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /anticodon=(pos:798. .800,aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .90, aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="codons recognized: CUY" /product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="codons recognized: CAR" /product="tRNA-Gln"
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/product="tRNA-Leu"
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/gene="trnL(uag)"
complement(1364. .1468)
/gene="psbM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55. .137
/gene="trnL(gag)"
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983. .1054
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/gene="trnQ(uug)"
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/gene="trnM(cau)"
1733. .3862
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/gene="trnM(cau)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332. .634
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/gene="rps14"
                                                                                                                                                     (bases 1 to 200799)
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Schudy,A., Blechschmidt,K., Schillhabel,M., Baumgart,C., Menzel,U.,
Weber,J., Schattevoy,R. and Rosenthal,A.
Direct Submission
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 109723) Schudy, A., Blechschmidt, K., Menzel, U., Polley, A., Reichwald, K., Rump, A., Schilbabel, M.B., Taudien, S., Wen, G., Schlegelberger, B., Siebert, R. and Rosenthal, A. Cisbert, R. and Rosenthal, A. Chromosome 8 genence Gunpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On Jun 1, 2000 this sequence version replaced gi:5514637.

* NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is the known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                     Submitted (06-JUL-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany 3 (bases 1 to 109723) Genome Sequencing Center Jena.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Nephroselmis olivacea chloroplast DNA, complete genome.
AF137379
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Chloroplast Nephroselmis olivacea
Eukaryota, Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
I (bases I to 200799)
Turmel,M., Otis,C. and Lemieux,C.
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2 62061: gap of unknown length
2 91746: contig of 29685 bp in length
7 109723: contig of 17877 bp in length.
Location/Qualifiers
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/note="assembly_fragment
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91647. .109723
/note="assembly_fragment
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Matches 20; Conservative
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complement(9442..9846)
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Chloroplast Nephroselmis olivacea
Chloroplast Nephroselmis olivacea
Chlorodendrales; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
1 (bases 1 to 200799)
1 (bases 1 to 200799)
1 (bases 1 to confident Lemieux, C.
Trumel, M., Otls, C. and Lemieux, C.
The complete chloroplast DNA sequence of the green alga
Nephroselmis olivacea: insights into the architecture of ancestral
                                                                                                                                                                                                                              /product="apocytochrome b6 of cytochrome b6/f complex"
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ROALLEGSVSVGGSTLTRFYSLHTFVLPLLTAVFMLHFLMIRKQGISGPL"
complement(90465.9431)
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AVPAGLLTVPFIESINKFQNPFRRPVATTVFLIGTVVAIWLGIGATLPIDISLTLGLF
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Proc. Natl. Acad. Sci. U.S.A. 96 (18), 10248-10253 (1999)
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Nephroselmis olivacea chloroplast DNA, complete genome.
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Turmel,M., Otis,C. and Lemieux,C.
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/gene="rps9"
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/gene="rp112"
                                                                                                                                                     .8779)
                                                                                   complement(8132. .8779)
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ilarity .90.9%;
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Direct Submission
Submitted (24-MAR-1999) Biochimie, Universite Laval, Pavillon
Charles-Eugene Marchand, Quebec GIK 7P4, Canada
Location/Qualifiers
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complement(1364. 1468)
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us-09-380-826a-7.rge

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Best Local Similarity 90.9%; Pred. No. 77;

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Search completed: March 27, 2001, 08:17:15 Job time: 5912 sec

Run on:

44: em_htg8:*

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21
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	120741 Sequence 6	I20742 Sequence 7	AR082373 Sequence	I52063 Sequence 5	I78419 Sequence 21	AX007639 Sequence	A88596 Sequence 74	A90563 Sequence 74	AR082368 Sequence	I78414 Sequence 21	AX007638 Sequence	AX007675 Sequence	A35660 Synthetic h	AR045297 Sequence	. AR071525 Sequence	I52349 Sequence 90		I61576 Sequence 13		I77301 Sequence 8	177302 Sequence 9
D	120741	120742	AR082373	152063	178419	AX007639	A88596	A90563	AR082368	178414	AX007638	AX007675	A35660	AR045297	AR071525	152349	161575	161576	161577	177301	177302
BB	81	81	81	81	82	19	81	81	81	82	79	79	81	81	81	81	81	81	81	82	82
% Query Match Length DB	11	11	13	13	13	14	14	14	14	14	15	15	15	15	15	15	15	15	15	15	15
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	7	7	7	7	7	7	. 7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
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Unclassified.
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1 (bases 1, C, Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Thompson, J.D.
HIV nef targeted ribozymes
Patent: US 5972704-A 217 26-OCT-1999;
Patent: US 5972704-A 217 26-OCT-1999;
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Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 217 from patent US 5972704..
8082773 AR082373.1 GI:10009099
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Sequence 5 from patent US 5646020.
152063
and applications thereof
Patent: US 5516634-A 7 14-MAY-1996;
Location/Qualifiers
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Unclassified.
Wases I to 11)
Newman, P.J. and Santoso, S.S.
Molecular basis of the human platelet bra/brb alloantigen system
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Unclassified.
I (bases 1 to 11)
Newman, P. J. and Santoso, S.S.
Molecular basis of the human platelet bra/brb alloantigen system and applications thereof
Patent: US 5516634 A 6 14-MAY-1996;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0;
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Sequence 7 from patent US 5516634.
120742 120742.1 GI:1601097
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Sequence 6 from patent US 5516634.
120741
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Unclassified.
1 (bases 1 to 14)
Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonucleotide preparation method
Patent: EP 0856579-A 05-AUG-1998;
BICGNOSTIK GES (DE)
Location/Qualifiers
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100.0%; Pred. No. 6.2e+05;
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Sequence 212 from patent US 5972704.
AR082368
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Sequence 744 from Patent EP0856579.
A90563 A90563.1 GI:6739077
Sequence 744 from Patent W09833904.
A88596
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/organism="unidentified"
/db_xref="taxon:32644"
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/db_xref="taxon:32644"
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                                                                                                                                                                                                            Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Thomson, J.D. Thomson, J.D. Thomson, J.D. Thomson, J.D. Patent: US 5693535-A 217 02-DEC-1997;
Location/Qualifiers
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100.0%; Pred. No. 6.2e+05;
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/db_xref="taxon:11966"
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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Aids-associated retrovirus
Viruses: Retroid viruses; Retroviridae.
1 (bases 1 to 14)
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Sequence 217 from patent US 5693535.
178419
178419.1 GI:3014573
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Sequence 181 from Patent WO9967428.
AX007639. GI:9995336
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Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
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Stuyver,L.
Method for detection of drug-selected mutations in the hiv protease
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Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
HIV targeted ribozymes
Patent: US 569355-A 212 02-DEC-1997;
Location/Qualifiers
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/organism="Aids-associated retrovirus"
/db_xref="taxon:11966"
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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6.2e+05;
Thompson, J.D.
HIV nef targeted ribozymes
Patent: US 5972704-A 212 26-OCT-1999;
Location/Qualifiers
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Sequence 212 from patent US 5693535.
178414
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Sequence 180 from Patent W09967428.
AX007638
AX007638.1 GI:9995335
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1 (bases 1 to 15)
Camble, R. and Edge, M.D.
Analogous interferon polypeptides, process for their preparation
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                                          Indels
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/db_xref="taxon:11966"
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/db_xref="taxon:32630"
4 c 2 g 4 t
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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Synthetic human IFN-alpha 2 gene oligo.
A35660
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Séquence 217 from Patent W09967428.
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H2-1 virus persistence-associated-gene 1 (PAG1) promoter uses therefor, and compositions containing same or products therefrom Patent: US 5911982-A 25 15-JUN-1999;
Location/Qualifiers
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0
                                                                                                              Unclassified.
Unclassified.
(bases 1 to 15)
Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 90 06-OCT-1998;
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Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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                              PAT
                         AR045297 15 bp DNA
Sequence 90 from patent US 5817796.
AR045297 GI:5966762
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Sequence 25 from patent US 5911982.
AR071525 GI:7222413
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Search completed: March 27, 2001, 08:17:04 Job time: 5901 sec

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    (without alignments)
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7991742 seqs, 3503743858 residues
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AZ484701 IM0311C24
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A1074857 Oy27b11.s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ386406 19 bp DNA GSS 02-0CT-2000
1M0145C22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0145C22 F, DNA sequence.
AZ386406
AZ386406.1 GI:10500106
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house mouse.
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TITLE

COMMENT

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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gblAF129072.1), a copy.number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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84112, USA
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                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                               1 (bases 1 to 20)

Unun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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/db_cref="tuxon:10090"
/clone="UGC1M0311C24"
/clone=lib="Mouse 10kb plasmid UGG1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0311 row: C column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center University of Utah Rm. 308 P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B.
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/note="Wector: PMOJANY: Purified genomic DNA from M.
musculus C578L/6J (male) was obtained from the Jackson
Labozatory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWDA2 (gill4)plA722012.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XILO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)

Unn, D., Adyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: '801 585 5606
Fax: 801 585 7177
Email: ddunn@enetics.utah.edu
meart Length: 10000 Std Error: 0.00
Plate: 0145 row: C column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends

    19 /organism="Mus musculus"
/strain="C57BL/6J"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 bNA polymerase and T4 polymucleotide kinase. Adaptor olignnucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcos get from a derivative electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil473211419D|RF129072.1), a copy-number inductorble derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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1M0350A24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0350A24 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /lab_host="Vector: PW042nv; Purified genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                  Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

10 (bases 1 to 21)

11 (bases 1 to 21)

12 (bases 1 to 21)

13 (bases 1 to 21)

14 (bases 1 to 21)

15 (bases 1 to 21)

16 (bases 1 to 21)

17 (bases 1 to 21)

18 (bases 2 to 21)
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 std Error: 0.00
Plate: 0249 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmld ends
High quality sequence stop: 21.
Location/Qualifiers
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/clone="UUGC1M0249E13"
AZ450829.1 GI:10606020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                           house mouse.
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Contact: Robert B. Weiss
Contact: y of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0249E13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0249E13 R, DNA sequence.
                                                                                                  Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

1 (bases 2 to 21)

1 (bases 2 to 31)

1 (bases 3 to 31)
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: A column: 17
Seq primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 21.
Location/Qualifiers
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/clone="UUGC1M0104A17"
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Fax: 801 585 7177
                                                                        house mouse.
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05-OCT-2000

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/organism="Homo sapiens"
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/lab_host="PH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone IMAGE:1667037 3' similar to TR:064507 Q64507 SERINE I ULTRA
HIGH SULFUR PROTEIN. ; contains PTR5 repetitive element ;, mRNA
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                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality lisert Length: 2304 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                          GI:3401501
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G0 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymoriectide kinase. Adaptor oligonoclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (414732114) pilAR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

University of Utah

84112, USA
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                                                                                                    Mus musculus

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Mayad. A., Marbach. T., Duval, B., Hamil, C., M., Rose, M., Rose, R., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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DEFINITION 0927b11.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0350 row: A column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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/clone="UUGC1M0350A24"
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AZ508369.1 GI:10689781
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Gaps 0;

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/organism="Mus musculus"
/strain="C57BL/6J"
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/strain="C57BL"
/db_ref="texon:1000"
/clone="ItheFE:1885092"
/clone="ItheFE:1885092"
/clone="ItheFE:1885092"
/clone="Lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 14 dpc"
/dev_stage="mbryo, 18 dpc"
/dev_d
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A1453394 GI:4281559
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
L Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Email: mouseestGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:969416
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Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
2E 1 (bases 1 to 26)
RS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Rose,R., Tingey,A., von Niederhausern,A.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
NL Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ352012 26 bp DNA GSS 29-SEP-2000 1M0090M13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0090M13 F, DNA sequence.
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194112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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100.0%; Pred. No. 1.6e+05;
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Insert Length: 10000 Std Error: 0.00
Plate: 0090 row: M column: 13
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence. stop: 26.
Location/Qualifiers
                                                                                                                                                                                            Trace considered overall poor quality
Insert Length: 1074 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 25
//organism="Homo sapiens"
//organism="Homo sapiens"
//clone="IMAGE:2143730"
//clone="IMAGE:2143730"
                                                                                                                                              www-bio.llni.gov/bbrp/image/image.html
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Mus musculus
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3 TGTTGGA 9
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                                                                                                            // Alachinoster. Coll Strain Allowoold, Tressignate, Franciscus Coll Strain Allowoold, Tressignate, Franciscus College, Male, was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TA DNA polymerase and TA polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwale (14732114) gphs/129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance.
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.
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                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                              /clone_lib="Mouse 10kb plasmid UUGClM library"
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100.0%; Pred. No. 1.6e+05;
ive 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/db_xref="taxon:10090"
/clone="UUGC1M0090Mi3"
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Location/Qualifiers
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AZ332711.1 GI:10396624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
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DEFINITION
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Laboratory Mouse DNR Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 gblAR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
RM: 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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/db_xref="taxon:10090"
/clone="UGCCIM0661N14"
/clone="UGCCIM0661N14"
/sex="Male"
/lab_nost="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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Insert Length: 10000 Std Brror:
Plate: 0196 row: N column: 03
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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Best Local Similarity 100...
7; Conservative
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Fax: 801 585 7177
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/organism="Mus musculus"
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Fax: 801 585 7177
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14 TGTTGGA 8
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AZ357647/C
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     source
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SOURCE
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                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubAl 1919[AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dipublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0062B09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0062B09 F, DNA sequence.
                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: B column: 09
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
/organism="Mus musculus"
/strain="C57BL/6J"
                                                   /db_xref="taxon:10090"
/clone="UUGC1M0196N03"
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Location/Qualifiers
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Best Local Similarity
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AZ333172/C
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/doares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polyworleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114) pblA129072.1), a copy-number. inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chancelly competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance.
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University of Utah Genome Center
University of Utah
Rm. 308, Blommedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Lalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M00GC1M0GC1B09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: D column: 19
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Class: plasmid ends
High quality sequence stop: 31.
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                                                                                                                                         /sex="Male"
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High quality sequence stop: 32.
Location/Qualifiers
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Fax: 801 585 7177
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Best Local Similarity
Matches 7; Conserv
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AZ328463
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                                                                                                                                                                                                                                                                                (http://www.fax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qiiq/32114 qib/AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0040P07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0040P07 F, DNA sequence.
AZ320254
AZ320254.1 GI:10371848
GSS.
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                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                               /organism="Mus musculus"
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Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0099D19"
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Fax: 801 585 7177
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AUTHORS
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114 qip.Hat129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah
RR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
RAI. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0052D18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0052D18 F, DNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Mus.
1 (bases 1 to 32)
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                                                                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                      /clone_lib="Mouse 10kb plasmid UUGCIM library"
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: D column: 18
Seg primer: CGTTGTAAAACGACGCCAGT
/organism="Mus musculus"
                                                                         /db_xref="taxon:10090"
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/clone_lib="Wouse lokb plasmid UGGIM library"
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/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
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musculus G57BL/G0 (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The Jackson
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from a gapprored bunt end in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 gb) AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                          /organism-"Mus musculus"
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Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
                                                                                                                                                                                                                    /strain="C57BL/6J"
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Search completed: March 27, 2001, 07:38:21 Job time: 4584 sec

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Gaps ; 0

Query Match 100.0%; Score 7; DB 170; Length 32; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 7; Conservative 0; Mismatches 0; Indels

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em_esthum10:*
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em_esthum13:*

em_esthum7: em_esthum8: em_esthum19:*
em_esthum20:*
em_estin1:*

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em_estpl1 em_estpl2

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em_estp15 em_estro1

em_estro2

em_estin2

em_esthum16:' em_esthum17:' em_esthum18:'

em_esthum15

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March 27, 2001, 07:38:17 ; Search time 2517.78 Seconds (without alignments) 61.230 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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em_estro12:

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em_estro8

gb_est73:*
gb_est74:*
em_esthum21:*
em_esthum22:*

gb_est67 gb_est68:

gb_est5;

gb_est70 gb_est71 gb_est72

gb_est69

gb_est53: gb_est54 gb_est55 gb_est56 em_estom1:

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υ			78.2	5/3	77	AI777095	AI	1777095 EST258060
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			78.2	619	97	AW963686	Š III	M903060 ES13/3/3/39 B57784 CIT-HSP-20
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[ (bases 1 to 361) Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                       The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chases 1 to 394)

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Contact: Desprez T., Amselem J., Chiapello H., Rouze P., Caboche
                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Arabidopsis thaliana flower buds Columbia"
/tissue_type="flower buds"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226559 394 bp mRNA EST 31-MAY-1995 ATTS1651 Versailles-VC Arabidopsis thaliana cDNA clone VCVDH08 3' similar to Ribonuclease (RNS2), mRNA sequence.
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Route de Saint-Cyr, 78026 Versailles
Email: thierry@versailles.inra.fr.
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Magnollophyta; endicotyledons; core endicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 490)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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//d_xxef="taxon:3702"
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//clone_lib="Arabidopsis thaliana Above-ground organ from two to six-week old plants Columbia"
//tissue_type="Above-ground organ from two to six-week old plants
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AB038725 AB038725.1 GI:7212552
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DB 147; Length 394;
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/organism="Arabidopsis thaliana"
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Conservative
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AUTHORS
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Karabidopsis thaliana

Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

I (bassa 1 to 530)

Rang,X., Hillman,J., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Gorgone,G., Burns,D., Griffin,J., Moustoutoud,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Shah,S., Nobriga,A., Murry,L., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Arabidopsis thaliana Gene Expression MicroArray

Unpublished (1999)

Acontact. David Smoller, Ph.D.

Genome Systems, Inc., a wholly owned subsidiary of Incyte
                        1 (bases 1 to 527)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                            The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuékazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 527
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Arabidopsis thaliana aboveground organs two to
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II;
Brassicales, Brassicaceae, Arabidopsis.
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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Tel: 877-577-2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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/cultivar="Columbia Col-0"
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Pred. No. 36;
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Email: service@genomesystems.com.
Location/Qualifiers
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/clone="APZ32g06F"
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90.9%;
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Best Local Similarity 90.9
Matches 20; Conservative
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Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
Nutional Institutes of Health
6 Center Drive MSC 2215, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliverehelix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 66 row: h column: 08
Seq primer: MJ3RP1 reverse primer (ABI).
                                                                                                                                                                      /note_vector: pSpORT: Site_l: NotI; Site_2: SalI; cDNA library was derived from untrated inflorescence tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:11 peat - 7 moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. CDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors , digested with NotI, size-selected, and cloned into the NotI and SalI sites of the psPoRT vector."
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//dev_state="1-5 day adult"
//lab_host="SOLR (Stratagene)"
//note="Yorgan: testis; Vector: pBlueScript SK (Stratagene);
Site_1: Ecor I: Site_2: Xho I; Testes dissected from 1-5
day adult y[*] w[67c1]/Y males raised at 25oC. RNA
isolated using Trizol (Life Technologies) and a single
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/db_xref="taxon:3702"
/clone="701676656"
/clone="101674656"
/tissue_type="inflorescence"
/dev_stage="4 - 7 weeks"
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/sex="male"
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/strain="y[*] w[67c1]/Y"
/db_xref="taxon:7227"
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0; Mismatches
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Query Match

BASE COUNT ORIGIN

Best Local

Matches

ó Dρ RESULT 7 CNS02BWA/C

LOCUS

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

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/organism="Medicago truncatula"
/oultivar="qenotype Al7"
/db_xref="taxon:3880"
/clone="ps5c-4115"
/clone="ps5c-4115"
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/dev_stage="mixture of cotyledons from five days old plants and leaves obtained from two weeks old plants"
/lab_host="E. coli strain SOLR"
/lab_host="E. col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicoryledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
I (bases I to 600)
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BF006254/c
LOCUS BF006254 633 bp mRNA EST 06-OCT-2000
DEFINITION EST434752 DSLC Medicago truncatula cDNA clone pDSLC-40G21, mRNA
                                                                                                                                                                                                                                                                                         BEY434942 DSLC Medicago truncatula CDNA clone pDSLC-41J15, mRNA
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ESTs from Medicago truncatula leaves and cotyledons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: debbys@puccini.crl.umn.edu
Iniversity of Minnesota name: M275482e TIGR sequence name:
MTLBASGTK More Information is available at:
http://chrysie.tamu.edu/medicago
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0;
             Indels
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             1;
             Mismatches
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90.5%;
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                 RESULT
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
         CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNSO2BWA 934 bp DNA GSS 12-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
254C22 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurpterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurpterygii; Chenosquamata; Acanthomorpha; Eucanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon. 1 (bases 1 to 934)

1 (bases 1 to 934)
round of Poly(A)+ selection using Oligotex (Glagen). cDN
library constructed using Stratagene ZAP-cDNA syntesis
kit. Oligo dT-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a Single round of amplification pBlueScript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 934)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                      DB 138; Length 608;
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/db_xref="taxon:99883"
/clone="254C22"
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95.0%; Pred. No. 59;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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AL190387.1 GI:7828491
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Best Local Similarity
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Gaps

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FEATURES

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

JOURNAL

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AUTHORS

REFERENCE JOURNAL

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BASE COUNT

ORIGIN

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Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kodoka, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shiganco, Y., Shinayawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Nishiyama, Y., Wastover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer \{5^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute of Physical and Chemical Research (RIKEN), Genomic
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="802003zc12"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
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Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciences Center
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JOURNAL
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/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-; Site_l: EcoRI; Site_l: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of cotyledons of five days old plants and leaves of two weeks old plants. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Giapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda=ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                   Tracheophyta; Spermatophyta;
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                                                                                                                                                       Medicago truncatula
Eukaryota, Viitdiplantae; Embryophyta; Tracheophyta; Spermatophyta,
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 286)
Ronno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.)
                                                                                                                                                                                                                                                                                                         Gantt, J.S., Vance, C.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M275292e TIGR sequence name:
WTLAU47TK Wore information is available at:
http://chysie.tamu.edu/madicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                       1 (bases 1 to 633)
Fedorova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., V
Gonzales, M., B. and Ellis, L.
ESTs from Medicago truncatula leaves and cotyledons
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 1.2e+02;
O; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSLC-40621"
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
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403 TTGGGTCACAAGATTTGAT 421
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Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                        Eukaryotation stercoralis

Eukaryotation Metacos; Nematoda; Chromadorea; Rhabditida;

Panagrolaimoidea; Strongyloididae; Strongyloides.

El (bases 1 to 40?)

McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwoon, B., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R.

The Mashington Univ. Nematode EST Project, 1999

The Mashington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Poreset Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Strongyloides stercoralis"
/strain="Rhabditiform larvae obtained from gerbils"
/db_xref="taxon:6248"
/clone_lib="TBN55TM-SSR"
/clone_lib="TBN55TM-SSR"
/lab_host="xL-1 Blue MRF" (Stratagene); Site_l:
/note="vector: Lambda Uni-ZAP KR (Stratagene); Site_l:
ECORI, Site_2: Xho!; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils experimentally infected dogs. cDNA was constructed from experimentally infected dogs. cDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the Ecori site to the Xho! site. The library has an unamplified titer of 1 x 10E5 ptu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average libsert size of the unamplified library is 675 bp (range, 100-1700)."
                                           BES81720 407 bp mRNA EST 16-AUG-2000 kq51c07.yl TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar to WP_T19B10.2 CE16413 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
NIAID, NIH (tnutman@nlh.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 384.
Location/Qualifiers
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                                                                                                                                                                                       Strongyloides stercoralis.
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Matches 18; Conserv
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KEYWORDS
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Gueen Anne Avenue North, Seattle, WA 98109, USA
701 Gueen Anne Avenue North, Seattle, WA 98109, USA
701 Gloof 516-3887
701 Email: jWallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
701 Enail: jWallablility, please contact Pieter de Jong
701 Gloof Resources (http://apacpac.med.buffalo.edu/ordering_bac.htm)
702 Resear h Genetics (info@resgen.com). BAC end Web Server:
703 Plate: 642 row: J column: 9
704 Seq Primer: TY: J column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 11 others
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                   Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF082E04STIF1034 Developing stem Medicago truncatula cDNA clone NF082E04ST 5', mRNA sequence.
                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 529)
                                                                                                                                                                                                              scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 1.8e+02;
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/clone="Plate=642 Col=9 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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Unpublished (2000)
Contact: Dixon RA
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Location/Qualifiers
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94.78;
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601101323F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3493829 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The state of the s
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Zap; Contains a mixture of internodal stem segments" 149 c 133 g 203 t
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Pred. No. 1.9e+02;
0; Mismatches 1; Indels 0
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 674 Std Error: 0.00
Plate: 082 row: E column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
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/clone="NF082E04ST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Developing stem"
/tissue_type="stem"
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:3493829"
/clone_lib="NCI_CGAP_Lu29"
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/lab_host="DH108"
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94.78;
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Matches 18; Conservative
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BE283043
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TITLE
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/organism="Ceratopteris richardii"
/cultivar="Brogn"
/cultivar="Brogn"
/db_xref="texon:49495"
/clone="Cri2_2 Boy"
/clone="Cri2_2 Boy"
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/clone_lype="Gametophyte"
/coll_type="Spore"
/dev_stage="20 hours after germination initiation"
/note="Vector: pcMvSPORT6; EST sequence from cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after their germination had been initiated by white light."
33 a 158 c 214 g 232 t
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Ceratopteris richardii
Ceratopteris richardii
Embryophyta; Tracheophyta; Filicophyta;
Filicopsida; Filicales; Pteridaceae; Ceratopteris.
1 (bases 1 to 837)
Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.
Expressed sequence tags of cDNA clones from a C. richardii library
Unpublished (2000)
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                                                                                                                     Length 762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Roux 53,
Section of Molecular Cell and Developmental Biology
Nulversity of Texas
Biology Building. Room 16, Austin, TX 78712, USA
Tel: 512 471 4238
Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Plate: Cri2_7 row: B column: 04
Seg primer: SP6.
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providing samples: Gilbert Smith, NIH" 172 c 207 g 190 t
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0; Mismatches 1; 1
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Best Local Similarity 94.7
Matches 18; Conservative
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Nucleotide sequenc 165 rRNA gene from Bacillus species p 165 rRNA gene. Bo Root Stimulating B Burkholderia cepac Nitrospira 165 rDN 165 rDNA sequence Curtobacterium sp.

Segmented filament B. subtilis AS2 st 16S ribosomal RNA

Pseudomonas testos Eubacteria sp. 165 B. cereus almost c rRNA gene (Stp.aur Staphylococcus aur

16S rDNA gene frag 16S rDNA gene frag

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Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

megaterium ssp

Sphingomonas sp. coli MG1655

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New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for prophylactic or therapeutic treatment
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X77384
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Score

Result Š. us-09-380-826a-1.rng

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This sequence represents a Leptospira DNA sequence isolated from the pathogonic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species limmunity against pathogenic LS bacteria can be used for conferring protective bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for prophylactic or therapeutic treatment of diagnosis of past or present LS infection.
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BP standard; DNA; 1535 (first entry) 21-DEC-1999 X83569 ~

sea water; detection; flagellum; Proteobacteria; glucose; carbon source; 16S rDNA gene fragment from marine bacterium, isolate K3-3. contamination; Monitoring; oil; contaminat Gram-negative bacterium; Pr Proteobacteria JP11243967-A.

> 999 099

X KENKYUSHO 98JP-0069399 98JP-0069399 KAIYO 04-MAR-1998; 04-MAR-1998; 14-SEP-1999 (KAIY-)

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nitoring of oil contamination of sea water - where oil contamination evaluated by detection of a microbe having properties from e.g. /ing no flagellum, being a Gram-negative bacterium, belonging to
                                   Proteobacteria, gamma subdivision, etc.2
                                                        3; Page 7-8; 15pp; Japanese
                         having
                                                        Claim
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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently a similate glucose as a single carbon source; and (5) it efficiently a fragment of the 16s rDNA gene from the microbe of the invention, isolate K3.3.

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Sequence 1535 BP; 375 A; 350 C; 496 G; 314 T; 0 other;
                            55.2%; Score 814.6; DB 20; 76.0%; Pred. No. 1.6e-243; iive 0; Mismatches 319;
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The invention relates to a new method for the production of taxane and paclitaxel compounds that comprises culturing bacteria isolated from a bacteria. The methods can be used for the production of taxanes such species of Taxus or bacteria produced by mutating the isolated bacteria. The methods can be used for the production of taxanes such as paclitaxel, 10-deacetylcephalomannine, 7-epitaxol, 10-deacetyl-baccatin 11, cephalomannine, 7-epitaxol, 7-xylosyl-baccatin 111, cephalomannine, taxaninine, delta-benzoyloxy taxadifine, 9-acetyloxy taxusin, 9-hydroxy taxusin, taxusin, 10-deacetyl-baccatin 111, raylosyl-taxadifine, 9-acetyloxy taxadifine, 9-acetyloxy taxadifine, 9-acetyloxy taxanel 10, tax
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Pred. No. 3.7e-243;
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                                                                                                                                                                                                                                                      The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10·30C n-alkanes. This sequence represents
                                                                                                                                                                                                                                                                                                         t least one of 10-30C n-alkanes. This sequence represents the 16s rDNA gene from the microbe of the invention,
                                                                                                                                                                                  litoring of oil contamination of sea water - where oil contamination evaluated by detection of a microbe having properties from e.g. ring no flagellum, being a Gram-negative bacterium, belonging to
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contamination; sea water; detection; flagellum;
terium; Protéobacteria; glucose; carbon source;
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                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.9
Best Local Similarity 76.2
Matches 1142; Conservative
Monitoring; oil; contamir Gram-negative bacterium;
                     16S rDNA gene;
                                                                                                                                                               WPI; 1999-564435/48.
                                        Proteobacteria
                                                                                                                                                                                                                                                                                                                   a fragment of isolate ST-T1.
                                                                                                                                            (KAIY-) KAIYO
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                                                             Pectate lyase; polysaccharide lyase; enzyme; pectin degradation; polygalacturonide; detergent composition; hard surface treatment; cellulosic fibre; plant material degradation; recycled waste paper; mechanical paper-making pulp; wine processing; ss.
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Kongsbaek L;
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                                         Bacillus pectate lyase rRNA sequence
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Glad SOS, K
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mannan; galactomannan; glucomannan; galactoglucomannan; cellulosic fibre; synthetic fibre; yarn; fabric; printing paste; thickener; viscosity; plant material degradation; recycled waste paper; paper making pulp; guar; locust bean gum; mannan-containing food; coffee extract; cleaning composition; machine washing; hard-surface cleaner; 165 RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the 16S RNA sequence of Bacillus Sp. AA112. This bacterium encodes a mannanse enzyme (also known as mannan endo-1,4-beta-mannosidase, beta-mannanase, or endo-1,4-mannanase). The mannanase hydrolyses galactomannans. Specifically, mannanases hydrolyses 1.4-beta-D-mannosidic linkages in mannans, galactomannans, plucomannans, and galactoglucomannans. The mannanase protein or preparations containing it, are used to improve properties of callulosic or synthetic fibres, yarn or (non)woven fabrics (removal of mannan-based
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                              ccgcccgtcacaccacctgagtggggagcacccgaagtggtctttgttaaccgta-agga
                                                                                                                                                                                                                                                                                                                         Mannanase; mannan endo-1,4-beta-mannosidase; beta-mannanase;
endo-1,4-mannanase; galactomannan; 1,4-beta-D-mannosidic linkage;
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sizes or printing pastes). They are also used to degrade or modify plant materials (particularly recycled waste paper, paper making pulps, or material containing quar or locust bean gums (thickeners), or to reduce viscosity of mannan-containing foods or feeds). The mannanases are also used to process coffee extracts (to inhibit gel formation); in cleaning compositions (for machine washing of fabrics, as hard-surface cleaners, for hand or machine dishwashing, also in oral, dental, contact lens or body-care compositions) where they remove mannan-containing soils and prevent binding of some soils to cellulosics; and in fabric softeners. They can also be used in oil well drilling to fracture
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Pred. No. 3.7e-242;
                                                                                                                                                                                                                                                                  Mismatches 303;
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                                        Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to Proteobacteria, gamma subdivision, etc. 2
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12 Score 810, DB 20;
76.2%; Pred. No. 4.3e-242;
Conservative 0; Mismatches 315;
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WPI; 1999-564435/48
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flagellum;
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                                                                          16S rDNA gene fragment from marine bacterium isolate Wf-1.
                                                                                            Monitoring; oil; contamination; sea water; detection; Gram-negative bacterium; Proteobacteria; glucose; cark alkane; 16S rDNA gene; ds.
                   вР
                                                         (first entry)
                   standard;
                                                                                                                                    Proteobacteria
                                                         21-DEC-1999
                 X83565
RESULT
          x83565
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14-SEP-1999

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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30C n-alkanes. This sequence represents a fragment of the 16S rDNA gene from the microbe of the invention, isolate Wf-1.
                                                                                                                                              contamination
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is evaluated by detection of a microbe having properties from e.
having no flagellum, being a Gram-negative bacterium, belonging
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Pred. No. 1.3e-241;
0; Mismatches 316; Indels
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nilarity 76.1%;
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98JP-0069399
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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30c n-alkanes. This sequence represents isolate Wf-2.

BP; 376 A; 352 C; 489 G; 312 T; 0 other;

Seguence 1529

Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to Proteobacteria, gamma subdivision, etc.z

Page 6; 15pp; Japanese.

Claim 3;

X

(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO

WPI; 1999-564435/48.

98JP-0069399 98JP-0069399

04-MAR-1998; 04-MAR-1998;

Proteobacteria

JP11243967-A

14-SEP-1999

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  Length 1529;
                   42;
                  Indels
Score 808.4; DB 20;
Pred. No. 1.3e-241;
0; Mismatches 316;
54.78;
76.18;
                 Conservative
        Best Local Similarity
Matches 1140; Conserv
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B. cereus BCM 4 partial 16S rRNA gene sequence

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The invention relates to a new method for the production of taxane and pacitaxel compounds that comprises culturing bacteria isolated from a plant species of Taxus or bacteria produced by mutating the isolated bacteria. The methods can be used for the production of taxanes such as pacitaxel, 10-deacetylcephalomannine, 7-epitaxol, 10-deacetyl-7-epitaxol, 7-epicephalomannine, baccatin III, 10-deacetyl-baccatin III, cephalomannine, taxagifine, delta-banzolyloxy taxagifine, 9-acetyloxy taxusin, 9-hydroxy taxagifine, delta-banzolyloxy taxane IC, or taxane IC (calmed). The taxane and paciltaxel compounds can be used for the taxanes and paciltaxel at a concentration of 1-25 mu g/l.
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                     cancer; 16S
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1513 BP; 387 A; 341 C; 467 G; 316 T; 2 other;
                    Taxane; paclitaxel; plant; bacteria; mutation;
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                                        Bacillus cereus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 76.9%; Score 805.4; DB 16; Length 1521; Matches 1097; Conservative 0; Minmaton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence corresponds to 16S ribosomal DNA from Bacillus sp
strain DSM 8721. This is a reference standard for isolation o
closely related strains (more than 92% sequence identity, or
preferably more than 93% identity of 16S ribosomal DNA) which
produce thermostable alkaline endo-1,4-beta-D-xylanase, which
is useful in paper production and pulp bleaching. The strain
itself produces such a xylanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                   thermostable alkaline endo-1,4-beta-D-xylanase

    useful in paper

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Beckhoven RFWC;
Williams DP;
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Jones BE, Quax WJ, Van
ij WA, Van Solingen P,
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                                                                                       ВР
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                                                                                       1521
                                                                                                                                                                                                   16S ribosomal DNA sequence
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                                                                                       DNA;
                                                                                                                                                                                                                                                                                         Bacillus sp. DSM 8721
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                                                                                       standard;
gtage 1512
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cacggtccagactcctacgggaggcagcagtagggaatcatccgcaatgggcgaaagcct
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This sequence represents the 16S rRNA gene of Pseudomonas cepacia strain KKOI. Fragments of the nucleic acid sequence (see TO1872-T03316) are useful as primers and probes for the specific detection of P.cepacia strain KKOI.
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                                                                                                                                                                                                                                                                                                                                                        Pseudomonas cepacia KKOl strain 165 rRNA gene - also related probes and primers, useful for specific detection of P.cepacia strain KKOl
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 805.4; DB 16;
Pred. No. 1.2e-240;
0; Mismatches 326;
                                                                                                                                             rRNA gene sequence.
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                                                                            BP
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                                                                                                                        (first entry)
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Matches 1124; Conservative
                                                                                                                                                                 16S rRNA; KK01; primer; F
detection; diagnosis; ds.
                                                                            DNA;
                                                                                                                                                                                                  Pseudomonas cepacia
                                                                                                                                                                                                                                                                                                                                   WPI; 1995-378541/49
                                                                            standard;
                                                                                                                                             P.cepacia 16S
                                                                                                                                                                                                                                                                                                             (CANO) CANON
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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently a ssimilates at least one of 10-30C n-alkanes. This sequence represents isolate TE-9.
                                                                                                                                                                                                                                                                                                                                                                                                                          Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to Proteobacteria, gamma subdivision, etc. 2
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                                                                                                                                                                                           nation; sea water; detection; flagellum;
Proteobacteria; glucose; carbon source;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1528;
rDNA gene fragment from marine bacterium, isolate TE-9.
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Pred. No. 1.5e-240;
0; Mismatches 325;
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Best Local Similarity 75.6%;
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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30C n-alkanes. This sequence represents a fragment of the 16S rDNA gene from the microbe of the invention, isolate K2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to
                                           gtcggaatcgctagtaatcgcggatcagaatgccgcggtgaatacgttcccgggccttgt 1379
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                                                                                 1403 aggagacagactactaaggtgaaactcgtaaagggggtgaagtcgtaacaaggtacc 1459
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                                                                                                                                                                                                                                                                                                         Monitoring; oil; contamination; sea water; detection; flagellum;
Gram-negative bacterium; Proteobacteria; glucose; carbon source;
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                                                                                                                                                                                                                                                                             16S rDNA gene fragment from marine bacterium, isolate K2-1.
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Pred. No. 1.5e-240;
0; Mismatches 325;
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                                                                                                                   Novel bacterial strain ADP (ATCC 55464), isolated from atrazine-contaminated soil, is capable of degrading s-triazine cpds., including atrazine. In an attempt to identify the strain, the 16S ribosomal RNA sequence (T18760) was compared to that of Escherichia coli (T18759), Pseudomonas citronellolis ATCC 15674 (T18761-63), Pseudomonas aeruginosa (T18764), Pseudomonas testosteroni (T18765) and Pseudomonas cepacia (T18766). It was concluded that ADP is closely related to, but distinct from, P. citronellolis and P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biologically pure culture of atrazine-degrading Pseudomonas - unto detoxify atrazine, e.g. in soil, at a wide variety of concus
                                                                                                                                                                                                                                                                    Atrazine; pesticide degradation; soil decontamination;
bioremediation; s-triazine; herbicide; ss.
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/note= "base 46 is identified as
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54.4%; Score 803.8; DB 17; 60.2%; Pred. No. 3.6e-240; ive 216; Mismatches 343;

Query Match 54.4%; Sc Best Local Similarity 60.2%; Pr Matches 897; Conservative 216;

Length 1536;

Oy Dp	1	gatcatggctcagaactaacgctggcggc-gcgtcttaaacatgcaagtcgagcgg 55	
δλ		ggtagcaatacctagcggcgaacgggtgagtaacacgtggtaatcttcctccga 10	on.
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; 셤	. 6	9999accuuc9g9ccuugugcuacuagagogcugauggcagauuagguaguggg 25	
٥y	230	taatggctcaccaaggcgacgatcggtagccggcctgagagggtgtccggccacaatg	0,
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٥y	290	agacacggtccatactcctacgggaggcagcagttaagaatcttgctcaatgg	o.
οqα	313	cugagacacggcccagacuccuacgggaggcaguggggaauuuuggacaauggg	8
οy	ĪΩ.	ccgcgtgaacgaaggtcttcggattgtaaagttcatt 40º : : :: : :	0
qq	373	aaagccugauccagcaaugccgcgugcaggaugaaggcccucggguuguaaacugcuu	7
à à	410	aggaaaaataagcagcaatgtgatgatgatacctgcctaaa	4 (
3	1	y uacyyaacygaaayeerayeeyyyy caaaaaceeeeeyyyy acyyyacyyyaacyyaaaaa 43,	N
Oy Dp	455 493	gcaccggctaactacgtgccagcagcggtaatacgtatggtgcaagcgttgttcgga 514	4 0
٥y	515	toattgggggtaaagggtgggtggggggtttgtaagtcaggtgtgaaaactgcggggc	4
qq	553	n illili	8
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Qγ	815	99	4
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οy	875	cggtggagcatgtggtttaattc	4
Og	913	gacgggacccgcacaagcgguggaugaugugguuuaauucgaugcaacgcgaaaaac	7
οy	935	atctgaatcatgta :	П
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ογ	6	ttcacaggtgctgcatggttgtcgtcagctcgtgtcgtg	
qq	3	acaggugcugcauggcugucagcucgugucgugagauguuggguuaagucc	
ò	1050	geaaccaacccctatectatectaecttaacttaactaccaacca	60

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Search completed: March 27, 2001, 08:22:56 Job time: 5298 sec

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Perfect score:

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

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APPLICANT: Herwig, Russell P.
APPLICANT: Stelefeldt, Angela R.
APPLICANT: Stenes, H. David
APPLICANT: Strand, Stuart E.
TITLE OF INVENTION: Degradation of Environmental Toxins by a TITLE OF INVENTION: Filamentous Bacterium
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Christensen O'Connor Johnson and Kindness PLLC 1420 Fifth Avenue, Suite 2800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/642,229A
US-08-632-470-41
US-08-632-470-29
US-08-632-470-45
US-08-632-470-47
US-08-632-470-47
US-08-632-470-31
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
TELEFAX: 4938023
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 base pairs
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0 ...
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,865
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
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DESCRIPTION: "16S ribosomal DNA"
HYPOTHETICAL: NO
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ADDRESSEE: Christens
STREET: 1420 Fifth A
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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Sequence 160, A
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Sequence 3, App
Sequence 1, App
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                                                                                                                                                                                              March 27, 2001, 06:53:33; Search time 132.3 Seconds
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US-08-114-695A-6
US-08-299-810A-27
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US-08-642-229A-2
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US-08-114-695A-1
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                            GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Score

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Result

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NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0057.00
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CLASSIFICATION: 425
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NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,9
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                                                          Score 814.2; DB 2;
Pred. No. 4.8e-284;
0; Mismatches 343;
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Best Local Similarity 74.7%;
Matches 1113; Conservative
US-08-642-229A-1
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                              caacgagcgcaaccctatcgtatgttgctaccttaagttgggcactggtacgaaactgc
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SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0, Version #1.30 APPLICANT: Jones, Brian E. TITLE OF INVENTION: ALKALI-TOLERANT XYLANASES NUMBER OF SEQUENCES: 20 Herbes, Wilhelmina T. Van Der Kleij, Wilhelmus A. Herweijer, Margaretha A. Van Beckhoven W.C., Rudolf F. Ouax, Wilhelmus J. SEE: Morrison & Foerster: 2000 Pennsylvania Avenue, Washington Sequence 20, Application US/08501126 Patent No. 6140095 GENERAL INFORMATION: Van Solingen, Pieter Williams, Diane P. Iverson, Sara Farrell, Roberta L. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible CORRESPONDENCE ADDRESS: OPERATING SYSTEM: 20006-1812 USA ADDRESSEE: 2

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APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mandelbaum, Raphael T.
APPLICANT: Wackett, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
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Patent No. 5508193
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TITLE OF INVENTION: WA
NUMBER OF SEQUENCES: E
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                               Length 1521;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                              54.5%; Score 805.4; DB 3; 76.9%; Pred. No. 7.3e-281; ive 0; Mismatches 292;
                                                                                                                                   ORGANISM: Bacillus sp.
INDIVIDUAL ISOLATE: DSM 8721
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 20: SEGUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                       Matches 1097; Conservative
                                                                          double
                                                              TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                             US-08-501-126-20
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                                                                                                                                                                     Length 1536
                                                                                                                                                                                           Indels
                                                                                                                                                                    Query Match 54.4%; Score 803.8; DB 1; Best Local Similarity 60.2%; Pred. No. 2.8e-280; Matches 897; Conservative 216; Mismatches 343;
 600.268US1
                                                                                                                           ; ORGANISM: Pseudomonas testosteroni
US-08-114-695A-7
REFERENCE/DOCKET NUMBER: 6
TELECOMONIOTATION INFORMATION
TELEDHONE: 612-339-0331
TELEFAX: 612-339-3061
                                                             LENGTH: 1536 base pairs
TYPE: nucleic acid
                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                    single
                                                                      TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
MOLECULE TYPE: rRNA
ORIGINAL SOURCE:
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Sequence 2, Application US/08995960
Sequence 2, Application US/08995960
Sequence 2, Application US/08995960
Sequence 3, Application US/08995960
Sequence 3, Application US/08995960
Sequence 3, Application US/08995960
Sequence 3, Application US/08995960
Sequence 2, Application US/089
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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CORRESPONDENCE ADDRESS:
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US-08-995-960-2
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APPLICANT: Kalser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 160, Application US/08757653
Patent No. 5843669
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                                                                                                                                                                                                                                                                                             Length 1512;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                             8; DB 3;
1.4e-279;
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/995 nc.
FILLIG DATE: 22-nc.
                                                                                                                                                                                                                                                                                            54.3%; Score 801.8; 75.3%; Pred. No. 1.46
                                                                                                                              34,235
                                                                                                                                     REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION
TELEPHONE: 617-523-3400
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
                                                                                                       ATTORNEY/AGENT INFORMATION
                                                                                                                  NAME: RESNICK, David S
REGISTRATION NUMBER: 34
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      Best Local Similarity 75.3
Matches 1134; Conservative
                                                                                                                                                                    TELEFAX: 617-523-6440
                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: rRNA
                                                                                              FILING DATE:
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                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                 Suite 2200
                                                                                                                                                                                             FORS-02565
                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COOS/MS-DOS
SOCTWARE: PALENTIN Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
                                                    America
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LL STREET: 220 Montgomery Street, CITY: San Francisco
                                                                                                                                              CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORSTELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 1555 base pairs
TYPE: nucleic acid
STRANBEDENES: double
                                                  United States Of
                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic)
US-08-757-653-160
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.3
Matches 1134; Conservative
                                                                    COMPUTER READABLE FORM:
                                         California
                                                                                                                                          FILING DATE:
                                                            94104
                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                 COUNTRY:
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US-09-248-528-2
Sequence 2, Application US/09248528C
; Patent No. 6153415
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APPLICANT: Padmakumar, Rugmini
APPLICANT: Kim, Sang H
TITLE OF INVENTION: Method for Producing Amide Compounds Using
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REFERENCE: MSU 4.1-401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09248528C Patent No. 6153415 GENERAL INFORMATION:
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APPLICANT: Oriel, Patrick J
APPLICANT: Oriel, Patrick J
APPLICANT: Padmakumar, Rugmini
APPLICANT: Rim, Sang H
ATTLE OF INVENTION: Method for Producing Amide Compounds Using a h
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REPERENCE: MSU 4.1-401
CURRENT APPLICATION NUMBER: 05/09/248,528C
CURRENT APPLICATION NUMBER: 60/083,485
EARLIER APPLICATION NUMBER: 60/083,485
EARLIER APPLICATION NUMBER: 50/083,485
SAFTURE RILING DATE: 1938-04-29
NUMBER OF SEQ ID NOS: 18
SOGTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1517
                                                                                                                                                                                                                                                                              Length 1517;
                                                                                                                                                                                                                                                                              53.6%; Score 792.4; DB 3;
llarity 75.0%; Pred. No. 3.7e-276;
Conservative 0; Mismatches 326;
                                                                                                                                                                                                    LOCATION: (1)..(1517).
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: 226929
DATABASE ENTRY DATE: 1998-07-02
                                                                                                                                                       TYPE: DNA
ORGANISM: Bacillus sy
FEATURE:
NAME/KEY: TRNA
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1128; Conserv
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                                                                                                                                                                                                              Length 1516;
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.2e-275;
es 327;
                                                                                    TYPE: DNA
ORGANISM: Bacillus pallidus
FEATURE:
NAME/KEY: FRNA
LOCATION: (1). (1516)
PUBLICATION: (1). (1516)
DATABASE ACCESSION NUMBER: 226930/GenBank
DATABASE ENTRY DATE: 1997-05-14
                                                                                                                                                                                                            Query Match
53.5%; Score 789.8; I
Best Local Similarity 75.0%; Pred. No. 3.2e-
Matches 1124; Conservative 0; Mismatches
  US/09/248,528C
CURRENT APPLICATION NUMBER: US/09/248,:
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 60/083,485
EARLIER FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mandelbaum, Raphael T.
APPLICANT: Wackett, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF S-
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WO
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; Patent No. 5508193
; GENERAL INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy
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US-08-114-695A-1
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GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States Of America
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STREET: 220 Montgomery Street, St
CITY: San Francisco
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Patent No. 5843669
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AuG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.268US1
TELECHONE: 612-339-0331
                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                       MOLECULE TYPE: rRNA ORIGINAL SOURCE:
                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                   SOURCE:
                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: lir
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                                                             gactigciggcicaaaacigacgcigaggcacgaaagcgigggiagiaacgggaitaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08114695A; Patent No. 5508193; GENERAL INFORMATION:
APPLICANT: Mandelbaum, Raphael T. APPLICANT: Wackett, Lawrence P. TITLE OF INVENTION: WATER; UMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                             52.8%; Score 780; DB 2; I 74.5%; Pred. No. 1.1e-271; ive 0; Mismatches 340;
                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/757,653
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                      FORS-02565
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUBBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-
TELECOMMUNICATION INFORMATION:
TELEPONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 158:
ENGTH: 1542 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-158
           Floppy disk
                                                                                                                                                                                                                                                                                            Query Match 52.8
Best Local Similarity 74.5
Matches 1116; Conservative
COMPUTER READABLE FORM:
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Sequence 1, Application US/08995960
Fatent No. 6030818
APPLICANT: PAGI, Michel
APPLICANT: LANDRY, Nathalie
APPLICANT: BOISSINOT, Maurice
APPLICANT: HILE, Marie-Claude
APPLICANT: HARVEY, Mario
APPLICANT: GAGNI, Mario
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.8%; Score 779.8; DB 1; Best Local Similarity 60.5%; Pred. No. 1.3e-271; Matches 876; Conservative 201; Mismatches 328;
                                                                                                                                                                                    600.268US1
                                                                                                                                                    NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPHONE: 512-339-031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             Pseudomonas cepacia
                                                                                                      31-AUG-1993
N: 435
                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: rRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                    linear
                                                                                                              FILING DATE:
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                 NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Dike, Bronstein, Roberts & Cushman, STREET: 130 Water Street
STREET: Boston
STRATE: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                      52.7%; Score 778.4; DB 3;
74.7%; Pred. No. 4.3e-271;
Live 0; Mismatches 336;
 BACTERIAL MASS PRODUCTION OF TAXANES AND PACLITAXEL
                                                                                                                COMPUTER: IBM Compatible
OPREATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     NAME: RESNICK, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 1826/47986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                    APPLICATION NUMBER: US/08/995,960 FILING DATE: 22-DEC-1997 CLASSIFICATION: 435 CLASSIFICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                     FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
TYPE: nucleic acid
                                                                        COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                        Diskette
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 INVENTION:
INVENTION:
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US-08-995-960-1
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Best Local Simi
Matches 1095;
TITLE OF
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373 AATGGGGGAAACCCTGATCCAGCAATGCCGCGTGTGAAGAAGGCCTTCGGGTTGTAAA 432
                                                   GCACTTTCGGTGGGGAAGAAATTCTCAAGGGTAATATCCTNGGGCGTTGACGTTACCCAC 492
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                                                APPLICANT: MABILAT, CLAUDE
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
CORRESPONDENCE AS
ADDRESSE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
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SCENERT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: US-08-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 772.6; DB 2;
Pred. No. 5.2e-269;
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEPHONE: (703)-836-6400
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           Sequence 53, Application US/08632470 Patent No. 5976791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic)
US-08-632-470-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.3%;
Best Local Similarity 74.1%;
Matches 1082; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                       GENERAL INFORMATION:
                                                                                                                                                                                                    USA
                                                                                                                                                                                                  COUNTRY: US ZIP: 22320
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                                                                                                   SOIL
                                                                                                   S-TRIAZINES IN
                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.2%; Score 770.6; DB 1; Best Local Similarity 59.6%; Pred. No. 2.8e-268; Matches 895; Conservative 203; Mismatches 367;
                                                                                            TITLE OF INVENTION: DEGRADATION OF S-TRIAZINI TITLE OF INVENTION: WATER NUMBER OF SEQUENCES: 8
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, STREET: 3500 IDS CENTER STREET: MINNEAPOLIS
STATE: MIN
                                                                                                                                                                                                                                                               SUFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
                                                                          APPLICANT: Mandelbaum, Raphael T. APPLICANT: Wackett, Lawrence P. TITLE OF INVENTION: DEGRADATION OF TITLE OF INVENTION: WATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        Sequence 6, Application US/08114695A Patent No. 5508193
                                                                                                                                                                                                                                                                                          FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION
TELEPHONE: 612-339-3061
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1518 base pairs
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                GENERAL INFORMATION:
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                             US-08-114-695A-6
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            AGCTTGCTTCTGATACTTAGTGGCGGACGGTGAGTAATGCTTAGGAATCTGCCTAGTAG
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CATARRHALIS
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                                                                                                                                                                                                                                                                                                                     #1.25
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Pred. No. 1.7e-267;
0; Mismatches 322;
                                                                                                            Sequence 27, Application US/08299810A
Patent No. 5721097
GENERL. INFORMATION:
GENERL. INFORMATION:
APPLICANT: Rossau, Rudi
APPLICANT: Van Heuverswyn, Hugo
TITLE OF INVENTION: BTECTION OF BRANHAMELLA (NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/299,810A
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.70-US-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                           ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5721097west Center
                                                                                                                                                                                                                               CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Branhamella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.0%;
Best Local Similarity 75.1%;
Matches 1075; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1485 base pairs
TYPE: nucleic acid
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CLONE: 16S rRNA Gene
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taatggctcaccaaggcgacgatcggtagccggcctgagagggtgtccggccacaatgga
                                                       tcattggggcgtaaagggtgcgtaggcggatttgtaagtcaggtgtgaaaactgcgggctc
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                                                                                  cagactactaaggtgaaactcgtaaagggggtgaagtcgtaacaaggtacc 1459
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Pred. No. 7.9e-267;
0; Mismatches 329;
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                      inch, 1.44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOLOGICAL NAME:
                                                                                                                                                                                                      APPLICANT: Kanta SAKAMOTO
TITLE OF INVENTION: DETECTION OF
NUMBER OF SEQUENCES: 21
                                                                                                                                                                   Sequence 21, Application US/08875445 Patent No. 5869642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , CECLOGY: linear
, MOLECULE TYPE: genomic DNA
, ORIGINAL SOURCE:
, ORIGINAL SOURCE: BIOLOGICAL N,
, ORIGINAL SOURCE: SPECIES NAME
US-08-875-445-21
                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
~wormer: IBM Compatible
MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REGISTRATION NUMBER: 40,949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/
FILING DATE: July 28, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.98;
74.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth,
STRRET: 805 Fifteenth
CITY: Washington
STRATE: D.C.
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Matches 1126; Conservative
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Search completed: March 27, 2001, 08:19:18 Job time: 5145 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
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                 Spermatophyta;
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta
Bugnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II
Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 800)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Gerldblyum, T., Lingng, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                           Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Fmail: attetigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
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/clone_lib="LERA"
/note="Organ: Leaf; Vector: pHOS1; Total genomic
sheared to 0.9-1 Kbp before ligation."
1 257 c 181 g 215 t
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Pred. No. 1.2e-127;
0; Mismatches 187; Indels 10;
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llarity 74.9%;
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

[ (bases 1 to 716)
Buell, C.R., Lin, X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Arabidopsis thaliana and identification of sequence-based
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for additional information, see http://www.tigr.org/tdb/at/at.html
Seg primer: TR
Class: shotgun.
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Pred. No. 1.3e-123;
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Contact: Xiaoying Lin
The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
Fax: 301 838 0200
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Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P.
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots, Rosidae, eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thallana genome survey sequence SP6 end of BAC T1
of TAMU library from strain Columbia of Arabidopsis thallana,
ALO93421
                                                                                 TGAAATCCCCGAGCTCAACTTGGGAACTGCGTTTGAAACTGCCAGACTAGAATATGTCAG
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                               attgtaaaagttcattaggcaggaaaaataagcagcaatgtgatgatggtacctgccta--
                                                 GTTGTAAAGCTCTTTCGCAAGGGAAGAAACTTACTTTCTAATAAÁGAGTGAGGCTGACG
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Submitted (25-JUN-1999) Genoscope - Centre I
BP 191 91006 EVRY cedex - FRANCE (E-mail : Web : www.genoscope.cns.fr)
Location/Qualifiers
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Arabidopsis thaliana
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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        CGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGCACATGT
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LERAP36TF LERA Arabidopsis thaliana genomic clone LERAP36, DNA
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Pred. No. 2.5e-118;
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Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 746)

Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T.,
Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
                                                                    polymorphisms
Unpublished (2000)
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9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TF
Class: shotgun.
                                                                                                                                                                                                                                                                                                 /clone_llb="LERA"
/rote="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
sheared to 0.9-1 Kbp before ligation."
153 c 225 g 159 t l others
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Pred. No. 1.8e-112;
0; Mismatches 181;
                                                                                                                                                                                                                      Location/Qualifiers
1. .746
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                              /strain="Landsberg erecta"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                        /clone="LERAP36"
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73.0%;
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Arabidopsis thaliana
Bukaryota; Usridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; endicotyledons; core endicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 741)
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Arabidopsis thallana and identification of sequence-based
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Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fal: 301 838 0208
Fax: 301 838 0208
Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
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LERAO33TR LERA Arabidopsis thaliana genomic clone LERAO33, DNA
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/note="Organ: Leaf; Vector: pHOSI; Total genomic DNA
sheared to 0.9-1 Kbp Defore ligation."
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Pred. No. 9.5e-111;
0; Mismatches 169; Indels
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74.6%;
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Class: shotgun
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719 TGGTGGAGTAAA 730
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Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 757)
Buell, C.R., Lin, X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERAO34"
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Tel: 301 838 0200
Fax: 301 838 0208
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Contact: Xiaoying Lin
The Institute for Genomic Research
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LERAO34TR LERA Arabidopsis
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Class: shotgun
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AQ957182.1
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                  Total genomic
                                                                                                                        DB 165; Length 757;
                                                                                                                                                         10;
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/clone_lib="LERA"
/note="Organ: Leaf, Vector: pHOS1; To Sheared to 0.9-1 Kbp before ligation. 3 247 c 170 g 203 t
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T27K4TR TAMU Arabidopsis thaliana genomic
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Pred. No. 3.2e-109;
0; Mismatches 167;
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             Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,
, Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
                                                     A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3 Uppublished (1997)
Other_GSSs: T27K4TF
Contact: Steve Rounsley
Department of Eukaryotic Genomics
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Pred. No. 1.6e-108;
0; Mismatches 155; Indels
                                                                                                                                                                USA
                                                                                                                                                                MD 20850,
                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD Tel: 301 838 0200 Fax: 301 838 0208 Email: rounsley@tigr.org Seq primer: M13 Reverse Class: BAC ends
                                                                                                                                                                                                                                                   High quality sequence stop: 676.
Location/Qualifiers
1. .676
                                                                                                                                                                                                                                                                                                          /strain="Columbia"
/db_xref="taxon:3702"
/clone="T27K4"
                                                                                                                                                                                                                                                                                                                                                    /clone_lib="TAMU"
/sex="hermaphrodite"
1 (bases 1 to 676)
Rounsley, S.D., Field, C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.5%;
Best Local Similarity 76.2%;
Matches 515; Conservative (
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae, Arabidopsis.

(bases I to 693)

Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Arabidopsis thallana and identification of sequence-based
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/clone_lib="LERA19"
/clone_lib="LERA19"
/note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."
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                                                                           gtcgccaactcgcaagaggagctaatctctaaaagtcggtcccagttcggattggggtc 1263
gaatcattgggcgtaaagggtgcgtaggcggatttgtaagtcaggtgtgaaaactgcggg 572
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LERAJ19TR LERA Arabidopsis thaliana genomic clone LERAJ19, DNA
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Uppublished (2000)
Contact: Alaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Fax: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
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/db_xref="taxon:3702"
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Arabidopsis thaliana

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Bassicales; Brassicaceae; Arabidopsis.

(bases I to 676)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,

Genomic survey sequencing of Landsberg erecta ecotype of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: at@tigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TF
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/organism="Arabidopsis thaliana"
/strain="Landsberg erecta"
/db_xref="Lexuson:3702"
/clone="Lexures"
/clone="Lexures"
/clone="Lexures"
/note="Lorgan: Lesg"
/note="Corgan: Lesg"
sheared to 0.4-0.7 Kbp before ligation."
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clone LERJR28, DNA
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TTCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAGAACACCAACGGCGAAAGCACTCT
                       gctggctcaaaactgacgctgaggcacgaaagcgtgggtagtaaaacgggattagataccc
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Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 839 0208
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Arabidopsis thaliana
Arabidopsis thaliana
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Bassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 659)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T., and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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LERROPOTF LERG Arabidopsis thaliana genomic clone LERUR90, DNA
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                       Gaps
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  165;
 .6; DB :
Score 359.6;
Pred. No. 4e-
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76.7%;
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                 Best Local Similarity 76.7
Matches 517; Conservative
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                                                                                     For additional information, see http://www.tigr.org/tdb/at/at.html Similar to A. thaliana chloroplast sequence (GB:AP000423) Seq primer: TF Class: shotgun.
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                                                                                                                                                                                                                                                                                                      629
                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                        /strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="lb=RR90"
/clone_lib=LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total/, sheared to 0.4-0.7 Kbp before ligation."
                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                     Score 356.6; DB 165; Lengtl
Pred. No. 3.6e-102;
0; Mismatches 139; Indels
                                         MD 20850, USA
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Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                             Location/Qualifiers
1. .659
                                                                                                                                                                                                                                                                                                    Query Match 24.1%;
Best Local Similarity 77.3%;
Matches 497; Conservative (
                                                                          Email: at@tigr.org
                                                                                                                                                       source
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COMMENT
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/tissue_type="pericarp" //tissue_type="red ripe" into the for 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato fruit tissue Compublished (1999)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
EST298662 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA AW221851
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/cultivar="TA496"
/db_xref="texon:4081"
/clone="clEN4113"
/clone_lib="tomato fruit red ripe, TAMU"
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ilarity 77.0%; Pred. No. 7.8e-101;
Conservative 0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
121: 864 656 4366
Fax: 864 656 4293
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1. .677
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Submitted (10-ocr-1999) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/O Kitasato
University; 1-15-1 Kitasato, Sagamihara 228-8555, Japan
(E-mail:hattoriéhgc.ims.u-tokyo.ac.jp, Tel:042-778-9923,
                                                                                                                 1309
                                                                                                                                                                                                                                  ggcggggatgacgtcaaatcctcatggcctttatgtccaggggccacacacgtgctacaat 1189
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                        361 GGCCGGGACAAAAGGGTCGCGATCCCGCGAGGTGAGCTAACCCCAAAAACCCGTCCTCAG
                                                                                                                 ttcggattggggtctgcaactcgaccccatgaagtcggaatcgctagtaatcgcggatca
                                                                                                                                                                                                                                               541 CTGGCCATGCCCGAAGTCGT-TACCTTAACCGCAAGGGGGGATGCCGAAGGCAGGCCT
                                                           ggccgatacagagggtcgccaactcgcaagagggagctaatctctaaaagtcggtcccag
                                                                                                                                             421 TTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCCGGTCA
                            GGTGAGGATGACGTCAAGTCATGCCCCTTTATGCCCTGGGCGACACACGTGCTACAAT
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Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1999) In press
2 (bases 1 to 616)
Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
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9
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0; Mismatches 119; Indels
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Homo sapiens
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/db_xref="taxon:9606"
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Local Similarity 78.9%;
les 468; Conservative (
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Matches 468
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ENKATYOLES, VITIGIOLANCE, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( (bases I to 675)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Arabidopsis thallana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: atétigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1347 accgcccgtcacaccaccaccgagtggggagcacccgaagtggtctttgttaaccgtaagga 1406
                                                                                                                                                                       1107 ctgccggtgacaaaccggaggaaggaggatgacgtcaaatcctcatggcctttatgtc 1166
                                                                                                                                                                                                                                                                                                                                                 1227 taatctctaaaagtcggtcccagttcggattggggtctgcaactcgaccccatgaagtcg 1286
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LERA Arabidopsis thaliana genomic clone LERAJ19, DNA
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                                                                                  agattcacaggtgctgcatggttgtcgtcagctcgtgtcgtgagatgttggggttaagtcc
                                         496 CGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCC
                                                                                                                                                                                                                                                                                   Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
TTel: 301 838 0200
Fax: 301 838 0208
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/db_xref="taxon:3702"
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/clone_lib="LERA"
/note="Organ: Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:6783998
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Arabidopsis thaliana
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Unpublished (2000)
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Class: shotgun
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AQ956297.1
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/dev_argage="Adult"
//dev_argage="Adult"
//note="Organ: testis: Vector: pucl8; Site_1: Smal; Site_2: Smal; Amin: library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue many and cDNA amplification were performed under low stringency conditions.

146 c 234 g 126 t lothers
                                                                                                                                                                                                          Fax: +55-11-270001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=&t2=QV0-TT0009-191
199-056-b02&t3=1999-11-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 659.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 taaacgggattagataccccggtaatccacgccctaaacgttgtctaccagttgtgggg 793 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 CGGTGTCTGGTCTGAGAGGATGATCAG-CACACTGGGACTGAGACACGGCCCAGACTCCT 71
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  97 (7), 3491-3496 (2000)
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                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 3.6e-98;
); Mismatches 156;
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/organism="Homo sapiens"
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/clone_lib="TT0009"
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ilarity 74.4%;
Conservative
                                                                                                                                                                                      Tel: +55-11-2704922
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1 (bases 1 to 659)

10 blas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW833978 659 bp mRNA EST 18-MAY-2000
QVO-TT0009-191199-056-b02 TT0009 Homo sapiens cDNA, mRNA sequence.
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                                                                                                   Score 346.8; DB 165; Lengt
Pred. No. 4.7e-99;
0; Mismatches 162; Indels
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73.8%;
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                                                                                                                                                        Matches 484; Conservative
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(bases 1 to 603)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                      Contact: Brika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Emall: asamizu'dkazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Arabidopsis thaliana flower buds Columbia"
/tissue_type="flower buds"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Infection; pathogenic Leptospira; protective immunity; therapy;

Leptospira fainei. WO9840099-A1.

diagnosis;

L. fainei nucleotide sequence

20-JAN-1999 (first entry)

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V58896 standard; DNA; 1477 BP

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               This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hursbridge or serovar hursbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
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(PIGR-) PIG RES & DEV CORP.
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(AGRI-) AGRIC VICTORIA SERVICES PTY LTD. (PIGR-) PIG RES & DEV CORP.

WPI; 1998-520791/44.

Chappel RJ;

98WO-AU00145. 97AU-0005494

06-MAR-1998; 07-MAR-1997;

17-SEP-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                           Nucleic acid encoding proteins involved in male fertility in plants - used to control fertility and for production of hybrid seed
Zm41-A; male fertility; hybrid seed; transgenic plant; antisense;
ribozyme; male sterile; maize; Ms41-A; ds.
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90.0%; Pred. No. 26;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassicaceae, lettuce, spinach and onlons
                                                                                                                                                                                                                                                       Perez P;
                                             Location/Qualifiers
823..915
/*tag= a
916..935
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268 TGTTGAATCACAAGATCTGA 249
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936..1090
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Best Local Similarity
Matches 18; Conserva
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemla; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schlorbenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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97US-0048881.
97US-0048884;
97US-0048893.
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                        V59636/c
  RESULT
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C encoding human secreted proteins (W88534 to W88756). The secreted protein

C gene sequences are deposited with the ATCC under deposit numbers ATCC

Gene sequences are deposited with the ATCC under deposit numbers ATCC

C 97979, 79794, 27976, 290603, 209004, 209009, 209010,

C 209011, 209080, 209081, 209083, 209084, 209085, 209511. Host

C 209011, 209080, 209081, 209083, 209084, 209085, 209511. Host

C 209011, 209080, 209081, 209083, 209084, 209085, 209511. Host

C 209011, 209080, 209081, 209083, 209084, 209085, 209511. Host

C 209011, 209080, 209081, 209083, 209084, 209085, 209511. Host

C 209011, 209080, 209081, 209083, 209084, 209085, 209511. Host

C 209011, 209080, 209081, 209083, 209084, 209085, 209511

C 2000111, 209080, 209081, 209083, 209084, 209085, 209511

C 2000111, 209080, 209081, 209083, 209084, 209085, 209084

C 3000111, 209080, 209081, 209081, 209083, 209084

C 3000111, 209080, 209081, 209081, 209084

C 3000111, 209080, 209081, 209081, 209084

C 3000111, 209080, 209081, 209081, 209084

C 4000111, 209080, 209081, 209081, 209084

C 4000111, 209080, 209081, 209081, 209084

C 400011, 209080, 209081, 209081, 209084

C 400011, 209080, 209081, 209081, 209084

C 400011, 209080, 209081, 209081, 209084

C 5001990910, 209081, 209081, 209081, 209081, 209088

C 5001990910, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 209081, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                             Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA, Fan P, Feng P, Ferrie AM, Flscher CL, Florence C; Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW; LI Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM; Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
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85.7%; Pred. No. 47
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97US-0057649.
97US-0057654.
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97US-0057760.
97US-0057763.
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                                        970S-0048963.
970S-0048971.
970S-0049019.
970S-0057627.
970S-0057634.
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97US-0057774
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97US-0048901
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06.JUN-1997;
06.JUN-1997;
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05.SEP-1997;
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05-SEP-1997
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemla; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                     Human secreted protein gene 126 clone HELGH31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             970S-0047582.
970S-0047583.
970S-0047584.
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970S-0047585.
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97US-0040626.
97US-0043311.
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97US-0040333.
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970S-0047595
V59636 standard; DNA; 1291 BP.
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                                       19-JAN-1999 (first entry)
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23-MAY-1997;
23-MAY-1997;
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                                                                                                                                                                   Homo sapiens.
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07-MAR-1997
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Gaps

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Pred. No. 47;); Mismatches

Query Match Best Local Similarity 85.7 Matches 18; Conservative

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Gaps

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209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Pc portion (e.g. v59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: v95311-v85012; amino acid sequences WW4731-W73056) which are useful for preventing, treating or ameliocating medical conditions e.g. by protein or gene therapy. Also, pathological conditions an be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V55511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polyeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in mannans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
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Pred. No. 48;
0; Mismatches
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97US-0050359.
97US-0053344.
97US-0053377.
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85.7%;
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                                                                                                                                                                                                                                        Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
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22-JUL-1997;
22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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 970S - 0047599

970S - 0047600

970S - 0047613

970S - 0047613

970S - 0047614

970S - 0047613

970S - 0048974

970S - 0056832

970S - 0056832

970S - 0056845

970S - 0056845

970S - 0056845

970S - 0056874

970S - 0056874

970S - 0056876

970S - 0056876

970S - 0056887

970S - 0056888

970S - 0056888

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970S - 0056889

970S - 0056889
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97US-0056910.
97US-0056911.
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97US-0057669
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06-JUN-1997;
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22-AUG-1997
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22-AUG-1997
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23-MAY-1997
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VINU ( UNIW)
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                                                                                                                                                                                                                                                                                                        Maize acetyl
                                                                                                                                                                                                                                                                                 23-JAN-1997
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Wyse DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         produ.
                                                                                                                  Query Match
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                                                                                                                                                                                                                                                               T39904;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence encodes a maize acetyl-CoA-carboxylase (ACCase, EC-6.1.2) fragment. The enzyme catalyses the formation of malonyl-CoA from acetyl-CoA and bicarbonate, and requires a biotin malonyl-CoA from acetyl-CoA and bicarbonate, and requires a biotin prosthetic group for activity. The enzyme is inhibited by several prosthetic group for activity. The enzyme is in monocotyledons. The herbicides (e.g. fluazifop and sethoxydim) in monocotyledons. The sequence is a 2-kb EcoAI fragment of phage lambda-gtll clone 15-14, solated from amize-inbred A188 seedling cDNA library by transcarboxylase active site domain (T17112) and the biotin binding transcarboxylase active site domain (T17112) and the biotin binding site domain (T17113) coding sequences may be used to screen plants site domain (T17113) coding sequences may be containing the gene, a for similar genes. An expression cassette containing the gene, a mutant or an antisense DNA sequence may be combined with a plant
                                                          Gaps
                                                                                                                                                                                                                                             Malze; acetyl-CoA-carboxylase; fluazifop; sethoxydim; herbicide; probe; transcarboxylase active site; biotin binding site; probe; transit peptide; plasmid; screening; cassette; antisense; promoter; transit peptide; plasmid; tissue-specific gene expression; herbicide resistance; oilseed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression cassette containing plant acetyl CoA gene - used to confer herbicide tolerance or to increase oil content of plants
                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= Transcarboxylase active site region
59..70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somers DA;
                                     Length 1473;
                                                            Indels
    sequence 1473 BP; 622 A; 232 C; 121 G; 498 T; 0 other;
                                                                                                                                                                                                                                                                                            oil content; transgenic plant; crop improvement; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lutz SM,
                                        20;
                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                       /product- Biotin binding site
                                        DB
                                       Score 16.2; 1
Pred. No. 49;
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gronwald JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 35-38; 31pp; English.
                                                                                                                                                                                                                                Acetyl-CoA-carboxylase gene fragment.
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1770..1946
/*tag= a
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90US-0538674.
92US-0917462.
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                                                                                                                                                                 T17111 standard; DNA; 2000 BP
                                                                                                          68 GCTGCATCACAGGATTTGATA 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88US-0269584
                                          73.6%;
85.7%;
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Wyse DL;
                                                                                                                                                                                                              (first entry)
                                                                                        2 gttggatcacaagatttgata
                                              Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               portion of a maize acetyl con carboxylase (ACCase) gene located at portion of a maize acetyl codo carboxylase (ACCase) gene located at bases 2883 to 83 from the 3' stop codon. Clone #15-14 was isolated from a lambda gtil cDWA library of maize inhored Al88 seedlings by from a lambda gtil cDWA library of maize inhored Al88 seedlings by screening with maize ACCase and isolated. Other ACCase DNA fragments screening with maize accamplete cDNA (739905) coding for ACCase (W05590) have also been isolated. ACCase DNA can be incorporated into a vector and used to increase the herbicide tolerance or oil into a vector and used to increase the herbicide tolerance or oil heterologous systems.
                                                                                                                                                                                                                                                                                                                                      Gaps
promoter, e.g. a cauliflower-mosaic virus 35S promoter or mopaline-synthase promoter, and N-terminal maize chloroplast transit peptide sequence in a plasmid vector for high-level tissue-specific gene expression, to confer herbicide resistance and/or alter the oil content of the plant, or to increase the plant and/or alter the oil content of the plant, or to increase the plant and vectors yield, so that the crystallized ensyme may be used to screen and identify other herbicides that bind to and inhibit the ensyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A 2 kb EcoRI fragment (739904) of lambda clone #15-14 includes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding maize acetyl coenzyme A carboxylase gene - used for
in. of plants with herbicide tolerance or altered oil content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetyl CoA carboxylase; ACCase; herbicide tolerance;
cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil;
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                                                                                                                                                                                                                                                                                   Length 2000;
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                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COA carboxylase cDNA clone EcoRI fragment.
                                                                                                                                                                                                            Sequence 2000 BP; 546 A; 406 C; 494 G; 554 T; 0 other;
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                                                                                                                                                                                                                                                                                             17;
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pred. No. 51;
0; Mismatches
                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                             73.6%; Score 16.2; 1
85.7%; Pred. No. 51;
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 18; Conserv
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Matches 18; Conser
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ò g BP.

(first entry)

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Mycobacterial DNA gyrase precursor protein - and polypeptide(s) corresponding to mycobacterial DNA gyrase intein sequences
                                                                                                                                                                                  Mycobacterium sp.; internal sequence; intein; immature; gyrase; protein splicing; precursor; gyrA; ss.
                                                                                                                                               M. leprae gyrA precursor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Pages 33-34; 55pp; French
                                   T64683 standard; DNA; 3822
                                                                                                                                                                                                                                        Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                                                                               17-0CT-1995;
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                                                                       T64683;
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 RESULT 11
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                    T64683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oil content
                                                                                                                                                                                                                    EcoRI fragment of lamda clone #15-14 with maize ACCase gene portion.
                                                                                                                                                                                                                                                                     maize acetyl CoA carboxylase; ACCase; herbicide; plant oil content; marker-assisted plant selection; groat oil trait; restriction fragment length polymorphism mapping; high-energy animal feed; low-fat human food; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Somers DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2001;
                                                                                                                                                                                                                                                      Herbicide resistance; gene modification; lamda clone #15-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rines HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               food and in genetic dissection of the groat oil trait.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2001 BP; 546 A; 406 C; 494 G; 554 T; 1 other;
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Best Local Similarity 85.7%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches
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EGLI M A.
GROH S.
42 gttggatgacaagagttgtta 62
                                                                                                          Z49816 standard; DNA; 2001 BP
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                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KIAN') KIANIAN S F.
(PHIL') PHILLIPS R L.
(RINE') RINES H W.
(SOME') SOMERS D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147205/13.
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02-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USDA )
(EGLI/)
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                                                                                                                                              249816;
                                                                       RESULT
Z49816
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95FR-0012162. 95FR-0012162.

Fsihi H;

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This DNA, isolated from Mycobacterium leprae, encodes a precursor during the protein from which an "intein" (see M15074) is excised during maturation. The gyrase and its coding sequence are useful to fabricate products that alter the maturation of proteins essential for the development of infectious agents by altering the protein splicing of precursor polypeptides of the proteins. W. flavescens, M. gordonae and M. kansasii are used: (a) to modify the genome of a eukaryotic cell that lacks endogenous biological activity identical to that of the polypeptide; (b) to replace a copy of a gene present in a recipient genome by integration of a gene different from that where the integration takes place; and (c) for targetted insertion of a foreign DNA sequence into a selected site in the genome of a eukaryotic cell not containing the specific cleavage sites of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3822 BP; 843 A; 899 C; 1092 G; 988 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.2; DE
Pred. No. 54;
0; Mismatches
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85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A3 maize ACCase cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q42933 standard; DNA; 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 gttggatcacaagatttgata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conserv
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Gaps

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Indels

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2 gttggatcacaagatttgata 22

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Acetyl COA carboxylase; ACCase; herbicide tolerance; cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil; oilseed; maize; corn; SS.

Maize acetyl CoA carboxylase cDNA.

23-JAN-1997 (first entry)

T39905;

Location/Qualifiers 37..7014 /*tag= a /EC_number= 6.4.1.2

WO9631609-A2

10-OCT-1996

Zea mays line A188.

902 gttggatgacaagagttgtta 922

T39905 standard; cDNA; 7470 BP

RESULT 13 T39905

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The sequence is that of the A3 acetyl coA carboxylase (ACCase) CDNA can alze clone which can be used to probe plant DNA to isolate other can maize clones. It may be used with plant regulatory sequences to produce expression cassettes for ACCase. These cassettes are used to produce expression cassettes for ACCase. These cassettes are used to the composition of seeds or other plant parts, e.g. enabling oil-content cobering plants such as oilseed rape, sunflower or oilpalm, having a lower or modified oil content to be produced. It can be used to form cassettes for overexpression of ACCase., leading to produce of plants with an increased oil content. It may also be used to form the ACCase expression of content. It may also be used to recover of plants with an increased oil content. It may also be used to recover cof plants with an increased oil content. It may also be used to recover correspectific or developmentally regulated manner, and this RNA in a correct of plants with a concept season of someocotyledonous plants can be made used to inhibit ACCase expression. Monocotyledonous plants can be made corresponded on a content to these herbicides such as fluazifor and alkylketones of transforming with cassettes adapted to expression of dicot achesived by overexpression of monocot ACCase. This is consibly by expression of a resistant form of maize ACCase. This correct term form of maize ACCase. This destroy weeds growing between the plants. This allows the overall destroy weeds growing the method, weeds such as wild oats may be previous crop. Using the method, weeds such as wild oats may be previous crop. Using means which are safer, cheaper or more effective.
Acetyl coA carboxylase; ACCase; probe; expression; oil content; lower; modified; increased; oilseed rape; sunflower; resistant; resistance; grass-weed herbicides; fluazifop; alkylketones; maize; wheat; barley; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA clones for use in probing plant DNA - comprise maize acetyl coenzyme-A carboxylase gene flanked by heterologous DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4346 BP; 1239 A; 829 C; 1064 G; 1213 T; 1 other;
                                                                                                                                                                                                                                                    /*tag= b
/note= "GAN encodes Glu or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suitable crops are maize, wheat and barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ICIL ) ICI AUSTRALIA OPERATIONS PTY LTD. (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashton AR, Jenkins CL, Whitfeld PR;
                                                                                                                                               Location/Qualifiers
3..3947
                                                                                                                                                                                       /*tag= a
/note= "ACCase"
1875..1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 3; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       92WO-GB02205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-197061/24
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                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1991;
                                                                                                                                                                                                                                                                                                              WO9311243-A.
                                                                                                                                                                                                                                                                                                                                                      10-JUN-1993.
                                                                                                                    Zea mays.
                                                                                                                                                            Key
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Somers DA;

Gronwald JW, Lutz SM,

Gengenbach BG,

Egli MA,

Wyse DL;

WPI; 1996-465030/46.

P-PSDB; W05590.

(MINU) UNIV MINNESOTA

95US-0417089

04-APR-1996; 05-APR-1995;

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                                                                                                                                                                                                                                                                                                                                                                                                                                            A CDNA sequence (T39905) codes for maize acetyl COA carboxylase (ACCase) (W05590), an enzyme that plays a central role in fatty acid biosynthesis and accumulation in plants and seeds. The complete sequence was deduced from CDNA clone #18-5, obto from a lambda gtll CDNA library of maize inbred A188 seedlings, and from PCR amplifications (see also T39918-23) Genomic ACCase DNA fragaments have also been isolated (see also T39906-16). ACCase DNA regaments have also been isolated (see also T39906-16). Accase DNA herbicide tolerance or oil content of a transgenic plant, or used
                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding maize acetyl coenzyme A carboxylase gene - used for prodn. of plants with herbicide tolerance or altered oil content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ed. No. 58;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%; Score 16.2; 1
85.7%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to produce ACCase in heterologous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 78-80; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3972 gttggatgacaagagttgtta 3992
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Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V29317;
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Gaps

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Indels

Query Match 73.6%; Score 16.2; ¹
Best Local Similarity 85.7%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches

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DB 14; Length 4346;

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Key

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Accase is involved in fatty acid synthesis and is the target of the specified herbicides. Transformation of plants with Accase imparts tessistance to cyclohexanedione and artyloxyphenoxypropanoic acid herbicides and alter the oil content. The Accase DNA is also used source of probes and primers for the identification of transgenic plants; in marker-assisted plants telection and for restriction fragment length polymorphism mapping, used for high-energy animal feed and high-fiber, low-fat human food and in genetic dissection of the groat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present CDNA sequence encodes maize acetyl CoA carboxylase (ACCase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oil content
                                                                                                                         maize acetyl CoA carboxylase; ACCase; herbicide; plant oil content; marker-assisted plant selection; groat oil trait; restriction fragment length polymorphism mapping; high-energy animal feed; low-fat human food; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7470 BP; 2119 A; 1430 C; 1843 G; 2071 T; 7 other;
                                                                                                                                                                                                                                                                                                                 /product= "Maize acetyl CoA carboxylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%; Score 16.2; D
85.7%; Pred. No. 58;
Live 0; Mismatches
                                                                                                          Herbicide resistance; gene modification;
                                                                                                                                                                                                                                                           Location/Qualifiers
37..7014
                                                                       Maize acetyl CoA carboxylase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Fig 13; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Egli MA, Groh S, Kianian SF,
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US DEPT OF AGRICULTURE.
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7014..7470
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                                  18-APR-2000 (first entry)
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Best Local Similarity 85.7
Matches 18; Conservative
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SOMERS D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGLI M A.
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02-JUL-1998;
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                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KIAN/) (PHIL/) (RINE/) (SOME/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MINU)
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249820;
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                                                                                                                                                                                                                                                           Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This cDNA encodes a maize ACCase enzyme. This can be used in a method of preparing an herbicide resistant corn plant which comprises crossing a first corn plant to a second corn plant so as to yield a progeny plant, where the first corn plant comprises at least 1 herbicide resistant allele which is not allelic to the herbicide resistant allele present in the first plant. The herbicide resistant corn plants are prepared using Acc1 and Acc2 gene combinations which impart cylcohexanedione (CHD) or aryloxyphenoxypropanoic acid (APA) herbicide tolerance to the corn plants. The methods are used to impart CHD entricide tolerance to corn plants and to produce CHD or APA herbicide tolerance to corn plants and to produce CHD or APA herbicide tolerance to a corn plants. Character and the methods can also be used to impart tolerance to a corn plant to an agent which inhibits acetyl COA carboxylase, selected from 3.(2.4-dichlorophenyl)-perhydroludolizine-2,4-dione, 3-isopropyl-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                     ACCase; maize; herbicide resistant; corn plant; tolerance; Accl; Acc2; cylcohexanedione; CHD; aryloxyphenoxypropanoic acid; APA; enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbicide resistant corn plants - prepared using Accl and Acc2 gene combinations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071 T; 7 other;
                                                                                                                                                                                                                                                         Ser)
                                                                                                                                                                                                                                         His)
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                                                                                                                                                                                                                                                         aa:
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                                                                                                                                                                                                              /*tag= a //transl_except= (pos:4339..4341, ./transl_except= (pos:4456..4458, i./transl_except= (pos:4359..4461, i./product= "ACCase"
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85.7%; Pred. No. 58;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Fig 3A-E; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM,
                                                                                                                                                                                 Location/Qualifiers
37..7014
/*tag= a
                                                      Maize ACCase enzyme encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Lutz SN
Wyse DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3972 gttggatgacaagagttgtta 3992
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                 (first entry)
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Best Local Similarity 85.7°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gengenbach BG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-207043/18.
P-PSDB; W56736.
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                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1997;
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                 30-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Somers DA,
                                                                                                                                                Zea mays.
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Somers DA;

Rines HW,

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Gaps

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Indels

3972 gttggatgacaagagttgtta 3992

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Z49820 standard; cDNA; 7470 BP

Z49820 ID Z4 XX

RESULT 15

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Length 7470;

DB 21; 3;

Search completed: March 27, 2001, 08:22:58 Job time: 5300 sec

us-09-380-826a-2.rng

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LENGTH: 2000 base pairs TYPE: nucleic acid
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COMPUTER READABLE FORM:
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STRANDEDNESS:
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STATE: MN
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US-08-014-326-1
Sequence 1, Appli
Sequence 5, Appli
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26.799 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
                                                                                                                                                                                           March 27, 2001, 08:19:18; Search time 132.3 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-244-537-1
US-08-417-089-5
US-08-695-651-5
US-08-684-862-8
US-08-792-055-1
US-08-299-675-1
US-08-874-162-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280836 segs, 80580151 residues
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    nucleic search, using sw model

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                                                                                                                                                                                                                                                                                  US-09-380-826A-2
22
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                      OM nucleic
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                                                                                                                                                                                              Run on:
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Appli
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     Sequence 1
Sequence 1
Sequence 3
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US-08-866-340-13
US-08-204-656B-1
US-08-204-656B-3
US-08-204-656B-5
US-08-204-656B-7
US-08-470-702-1
US-08-470-702-2
US-08-470-702-4
US-08-467-831-1
US-08-467-831-3
US-08-467-831-3
US-08-467-831-3
US-08-467-831-3
US-08-467-831-3
US-08-467-831-3
                                                                                                                                                           PCT-US94-02891-68
US-09-022-461-1
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GENERAL INFORMATION:

APPLICANT: Gengenbach, Burle G.

APPLICANT: Somers, David A.

APPLICANT: Week, Donald L.

APPLICANT: Egli, Margaret A.

APPLICANT: Egli, Margaret A.

APPLICANT: Latz, Shiela M.

TITLE OF INVENTION: Method and An Acetyl CoA Carboxylase
TITLE OF INVENTION: Alteration in Oil Content of Plants

CORRESPONDENCE: 4

CORRESPONDENCE: 4

CORRESPONDENCE: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,326
FILING DATE: 05-FEB-1993
CLASSIFICATION BOO
PRIOR APPLICATION BOO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,462
FILING BAPLICATION DATA:
APPLICATION NUMBER: US 07/917,462
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,674
FILING DATE: 18-JUN-1990
PRIOR APPLICATION NUMBER: US 07/538,674
FILING DATE: 18-JUN-1980
APPLICATION NUMBER: US 07/269,584
FILING DATE: 10-NOV-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,848
FR: 600.258-US01
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5498544west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kowalchyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 600.2
Sequence 1, Application US/08014326; Patent No. 5498544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         612-332-9081
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RESULT
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FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Somers, D. A.
APPLICANT: Wyse, D. L.
APPLICANT: Gronwald, J. W.
APPLICANT: Egl1, M. A.
APPLICANT: Lutz, S. M.
TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COA
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
T: P.O. Box 2938
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2001 Dase pairs
TYPE: nucleic acid
TYPE: single
                                                                                                                                DB 1;
                             : IMMEDIATE SOURCE: ... (Journal); CLONE: 2 kb fragment of lambda clone #15-14 US-08-014-326-1
                                                                                                                             Score 16.2; Di
Pred. No. 20;
0; Mismatches
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85.7%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      US-08-417-089-1

Sequence 1, Application US/08417089

Patent No. 6069298

: GENERAL INFORMATION:

APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08695651
; Patent No: 6146867
; GENERAL INFORMATION:
                                                                                                                                                                  0
linear
E: DNA (genomic)
                                                                                                                                                                                                     gttggatcacaagatttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gengenbach, B. G.
                                                                                                                             73.6%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METH
TITLE OF INVENTION: FOR
TITLE OF INVENTION: OIL
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
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Best Local Similarity 85.7
Matches 18; Conservative
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
   TOPOLOGY: 13
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US-08-695-651-1
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APPLICANT: JENKINS, COLIN L.D.
APPLICANT: WHITFELD, PAUL D.
TITLE OF INVENTION: MAIZE ACETYL COA CARBOXYLASE ENCODING
TITLE OF INVENTION: DNA CLONES
TITLE OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,537
FILING DATE: 18-AUG-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.6%; Score 16.2; I
Best Local Similarity 85.7%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: EASLED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIFICCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERNCE/DOCKET NUMBER: 600.318US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB 9125330.2
                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             APPLICATION NUMBER: 08/417089
FILING DATE: 05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08244537
Patent No. 5854420
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 GTTGGATGACAAGAGTTGTTA 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-695-651-1
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Sequence 14, Application US/08602145
Sequence 14, Application US/08602145
Sequence 14, Application US/08602145
Sequence 14, Application
GENERAL INFORMATION:
APPLICANT: Greenberger, Joel S.
TITLE OF INVENTION: DETERNINING EXPOSURE TO IONIZING RADIATION
TITLE OF INVENTION: AGENT WITH PERSISTENT BIOLOGICAL MARKERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7470;
                                              APPLICANT: Lutz, S. M.
TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COA
                                                                                                                                              Lundberg, Woessner & Kluth, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDESSEE: Foley & Larune,
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                          YSTEM: DOS
FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08/417089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-APR-1995
APPLICATION NUMBER: 08/014326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07/917462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07/538674
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917
FILING DATE: 21-UU-1992
APPLICATION NUMBER: 07/538
FILING DATE: 18-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.68;
85.78;
            Wyse, D. L.
Gronwald, J. W.
Egli, M. A.
Lutz, S. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 7470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 gttggatcacaagatttgata
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                              E: Schwegman,
P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          612-339-3061
                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                   Minneapolis
                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                          USA
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; MOLECULE TYPE:
US-08-695-651-5
                                                                                                                                                                                                                                          55402
                                                                                                                                                                                                                                                                                                       COMPUTER:
                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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PRIOR PAPLICATION DATA:

PRIOR PAPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/02205

FILING DATE: 27 NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REGISTRATION NUMBER: 203094/SEE 36663/UST

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEPA: 6714627 CU81

TELEPA: 6714627 CU81

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
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85.7%; Pred. No. 23;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%; Score 16.2;
85.7%; Pred. No. 22;
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08417089 Patent No. 6069298
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Patent No. 6146867
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-244-537-1
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic)
US-08-417-089-5
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                                                                                                                                                                                                                                                               LENGTH: 4345 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.0 Best Local Similarity 85.7 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.6'
Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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US-08-417-089-5
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SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,055
FILING DATE: 03-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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81.8%; Pred. No. 37;
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                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,361
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08792055 Patent No. 5853980,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rollin, Pierre E.
APPLICANT: Elliott, Luanne
APPLICANT: Riazek, Thomas G.
APPLICANT: Nichol, Stuart T.
APPLICANT: Norunco, Sergey
APPLICANT: Ravkov, Eugeny
TITLE OF INVENTION: The Black C.
ITILE OF INVENTION: Related Met.
NUMBER OF SECUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
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(404) 688-9880
OR SEQ ID NO: 1:
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                       SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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Matches 18; Conservative
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STRANDEDNESS: double
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STATE: Georgia
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INFORMATION FOR
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APPLICANT: Bach, Heinz
APPLICANT: Hillen, Heinz
APPLICANT: Bialojan, Siegfried
TITLE OF INVENTION: No. 5799541el Proteins, the Preparation and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCE: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kell & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: EM PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,145
FILING DATE: 15-FEB-1996
ATTONNEY/AGENT INPORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 076333/0112
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION
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MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
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APPLICATION NUMBER: US/08/684,862
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81.8%; Pred. No. 31
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APPLICATION NUMBER: 07/966,040
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: PCT/EP91/01361
FILING DATE: 19-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,705
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Patent No. 5759541
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399
TELEX: 904136
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 TTTTGCATCATAACATTTGATA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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Best Local Similarity 81.8
Matches 18; Conservative
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                                               20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE:
US-08-602-145-14
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Gaps
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COTATION: 144 to 841

COTHER INFORMATION: the coding region shown in (2)(ix)(B)

CHER INFORMATION: codes for the protein of SEQ ID NO: 3

US-08-684-862-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Black Creek Canal Hantavirus and
Related Methods
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,162
FILING DATE: 13-UN-1997
CLASSIFICATION: 435
                                                                                                                                                                                PC-DOS/MS-DOS
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                                                                                                                                          E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) US-08-485-241-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.9%;
81.8%;
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LENGTH: 7745 base pairs
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Best Local Similarity 81.8
Matches 18; Conservative
                                                                                   COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY di
COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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CORRESPONDENCE ADDRESS
                              STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                Length 1989;
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                                                                                                                                                                                                                              Sequence 1, Application US/08299675
Patent No. 5589618
GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: GIroux, Michael
APPLICANT: GIroux, Michael
APPLICANT: OF INVENTION: Materials and Methods for Increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-485-241-1/c

Sequence 1, Application US/08485241

Sequence 1, Application US/08485241

GENERAL INFORMATION:

APPLICANT: Hannah, L. Curtis

APPLICANT: Giroux, Michael

TITLE OF INVENTION: Materials and Methods for Increasing

TITLE OF INVENTION: Corn Seed Weight

NUMBER OF SEQUENCES: 5
                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,675
FILING DATE:
                                                                    4
                                DB 2;
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                70.9%; Score 15.6;
81.8%; Pred. No. 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.9%; Score 15.6;
81.8%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF146
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TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7745 base pairs
                                                                  18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 18; Conserva
                              Query Match
Best Local Similarity
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US-08-299-675-1/c
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                                                                    Matches
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Gaps
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Patent No. 5872216
GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
TITLE OF INVENTION: Materials and Methods for Increasing
TITLE OF INVENTION: Corn Seed Weight
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.6;
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,675
FILING DATE: 1-SEP-1994
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
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69.18;
85.08;
                                                               Query Match
Best Local Similarity 85.09
Matches 17; Conservative
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STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ttggatcacaagatttgata
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                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 17; Conserv
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ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GODWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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           US-08-399-9868-3
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TITLE OF INVENTION: No. 5801041el Gene Associated with Suppression
TITLE OF INVENTION: of Tumor Development
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,986B
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
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81.8%; Pred. No. 46;
tive 0; Mismatches
                 FILING DAIL.

CLASSIFICATION 435

PILOR APPLICATION DATA.

APPLICATION NUMBER: US 08/299,675

"TILING DATE: 1-SEP-1994
 JMBER: US 08/485,241
7-JUN-1995
                                                                     APPLICALLO. ...

FILING DATE: 1-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: 38,261
REFERENCE/DOCKET NUMBER: UF-1/
TELECOMMUNICATION INFORMATION:
TELEPAN: 352-375-8100
TELEFAX: 352-375-8100
TELEFAX: 352-375-8100
TELEFAX: 352-375-8100
TELEFAX: 372-S800
SEQUENCE CHARACTERISTICS:
LENGTH: 7745 base pairs
LENGTH: 7745 base pairs
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Sequence 3, Application US/08399986B

Patent No. 5801041

GENERAL INFORMATION:
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NAME: Hegan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 563-4100
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tgttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-874-162-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Philadelphia
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No. 5821338el Gene Associated with Suppression
of Tumor Development
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No. 5801041el Gene Associated with Suppression
of Tumor Development
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    DB 1; Length 1016;
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                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
Score 15.2; i
Pred. No. 57;
                                            Mismatches
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85.0%; Pred. No. 57;
tive 0; Mismatches
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US-08-493-754A-3/C
US-08-493-754A-3/C
Sequence 3, Application US/08493754A
Patent No. 5821338
GENERAL INFORMATION:
APPLICANT: GODA'N, Andrew K.
TITLE OF INVENTION: No. 5821338e1 G
TITLE OF INVENTION: Of TUMOr Develc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-399-986B-1/c
; Sequence 1, Application US/08399986B
; Patent No. 5801041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
                                                                                                      830 TTGGGTCTCAAGAATTGATA 811
                                                                            3 ttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830 TTGGGTCTCAAGAATTGATA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 563-4100
TELEFRAX: (215) 563-4044
INFORMATION FOR SEO ID NO. 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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Query Match

69.1%; Score 15.2; DB 1; Length 2182;
Best Local Similarity 85.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 3; Indels 0;
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman STRET: 1601 Market Street
CTTY: Philadelphia STATE: PA
CCTY: Philadelphia STATE: PA
COUNTRY: USA
COUNTRY: USA
COMPUTER: DANA
COMPUTER: TEM PC COMPATION:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATION:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,986B
FILING DATE: 06-MAR-1995
CLASSIFICATION: TNFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARATTERISTICS:
LENGTH: 2182 base Pairs
TELEPHONES: double
TTELEPHONES: double
TTELEPHONES: double
TOPOLOGY: not relevant
MOLECULE TYPE: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
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Search completed: March 27, 2001, 08:19:19 Job time: 5146 sec

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Ouery Match
Best Local Similarity
Matches 7; Conserv
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US-08-631-751A-13
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COUNTRY:
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                                                                 March 27, 2001, 08:19:19; search time 132.3 Seconds (without alignments) 8.527 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1367,
Sequence 1729,
Sequence 1730,
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                                                                                                                                                                                                    561672
                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-585-684B-1768
US-08-585-684B-1769
US-08-585-684B-1770
US-08-585-684B-2139
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                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                280836 segs, 80580151 residues
                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
                                                                                                                                                                                                                       length: 0
length: 2000000000
                                                                                                   US-09-380-826A-4
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Match Length
                                                                                                                            1 tgttgga 7
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                                                                                                                     Perfect score:
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Maximum DB
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25, Appl
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5, Appli
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Sequence
Sequence
Sequence
US-08-281-940-25
US-08-390-850-433
US-08-374-124A-810
US-08-441-370-2
US-08-441-370-2
US-08-441-370-2
US-08-441-370-2
US-08-41-370-2
US-08-710-134-25
US-08-710-134-25
US-08-704-966-5
US-08-704-966-5
US-08-704-966-5
US-08-985-162-529
US-08-985-162-530
US-08-985-162-530
US-08-985-162-531
US-08-985-162-531
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US-08-479-939-47
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Microfabricated, Flowthrough Porous
Apparatus for Discrete Detection of Binding Reactions
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                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,751A
FILING DATE: 11-April-1996
CLASSIFICATION: 435
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5.1e+03;
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                                                                                                                                                 3: Vinson & Elkins
1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7;
Pred. No.
Sequence 13 Application US/08631751A
Patent No. 5843767
GENERAL INFORMATION:
APPLICANT: Beattle, Kenneth L.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFRENCE/CDOCKET NUMBER: HARC
TELEDOMMUNICATION INFORMATION:
TELEPHONE: (202)639-6500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10 base pairs
                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
                                                                       TITLE OF INVENTION:
                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 201, Application US/08182968A
Fatent No. 5610034
GERERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION:
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                             FILLING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILLING DATE: 27-JUN-1994
FILLING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
TELEPRAX: (212) 758-6849
INFORMATION FOR SED ID NO: 154:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: WORD PEFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A FILING DATE: 13-JANUARY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other nucleic acid /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/765,340 FILING DATE: 23-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                             ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Tr Conserve
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STATE: California
COUNTRY: U.S.A.
                                              NEW YORK
: NEW YORK
RY: USA
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                                                                                           COUNTRY:
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Sequence 19, Application US/08303004
Patent No. 5556955
GENERAL INFORMATION:
APPLICANT: Vergnaud, Gilles
TITLE OF INVENTION: Process for Detection of New Polymor-
TITLE OF INVENTION: phic Loci in an ADN Sequence, Nucleotide Sequences Forming
TITLE OF INVENTION: Hybridisation Probes and Their Biological Applications
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Rarrial-
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDE TON DATE: US/07/931,311B
FILING DATE: 19920818
ATTORNEY/AGENT INFORMATION:
NAME: BETINGOG WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1806MATION:
TELEFAX: (703) 836-2287
TELEFAX: (703) 836-2287
TELEFAX: (703) 836-2287
TELEFAX: 00-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 7; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 154, Application US/08765340; Patent No. 6150092; GENERAL INFORMATION:
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O
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P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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APPLICANT: UCHIDA, T.,
APPLICANT: TANAKA, Y.,
APPLICANT: MATSUDA, Y.,
APPLICANT: KONDO, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                  CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inear
                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: NO
US-08-303-004-19
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 TGTTGGA 6
                                            US-08-303-004-19/c
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US-08-765-340-154
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                                                                                                                                                                                                                                                                                STREET:
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STREET:

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Gaps
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                                                                                                                                                                                                                                                                              US-08-363-240A-614/C

Sequence 614, Application US/08363240A

Patent No. 5705388

GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwigen, James
APPLICANT: Bagaier, Charles
APPLICANT: Pape, Michael
ITILE OF INVENTION: METHOD AND REAGENT FOR
ITILE OF INVENTION: PROGRESSION AND REGRESSION
ITILE OF INVENTION: PROGRESSION AND REGRESSION
ITILE OF INVENTION: OF VASCULAR DISEASES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 7; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 7; Conservative 0; Mismatches 0;
                                                                       Query Match
100.0%; Score 7; DB 1; L.
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REBRENCE/COCKET NUMBER: 210/(TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 614:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tgttgga 7
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13 TGTTGGA 7
        US-08-182-968A-246
                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 7; DB 1; Length 15; Best Local Similarity 57.1%; Pred. No. 5.2e+03; Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NESOLI 82-968A-246/C
Sequence 246, Application US/08182968A
Patent No. 561006A
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPATITS C TITLE OF INVENTION: VIRUS REPLICATION NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 633 West Fifth Street STREET: Suite 4700
CITY: Los Angeles STREET: Galifornia COUNTRY: U.S.A.
ZIP: 90071-2066
COMPURY: U.S.A.
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTRANE: WARD PERFOCT 5.1
CURRENT APPLICATION NAMBR: US/08/182,968A
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
RPLICATION NAMBR: 07/882,888
FILING APPLICATION NAMBR: ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION UNDBER:
FILING DATE: 14-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: WATBURY, RICHARD:
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JABER: 21

JAEFAX: (213) 489-1600

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 UGUUGGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tgttgga 7
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Length 15;
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Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPATITIS C TITLE OF INVENTION: UNRUS REPLICATION NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 7; DB 1; 100.0%; Pred. No. 5.2e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                         COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOR'D PERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: December 26, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard
RECISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 TGTTGGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tgttgga 7
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-363-240A-616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-774-306A-201
                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7; DB 1; Length 15; 100.0%; Pred. No. 5.2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                            APPLICANT: MCSWiggen, James
APPLICANT: Bisgaier, Charles
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREVENTION, INHIBITION OF
PROGRESSION AND REGRESSION
OF VASCULAR DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHOD AND REAGENT FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 616, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Pasgaier, Charles
APPLICANT: Page, Michael
TITLE OF INVENTION: PREYENTION, INHIB
TITLE OF INVENTION: PROSESSION AND R
TITLE OF INVENTION: OF VASCULAR DISEA
NUMBER OF SEQUENCES: 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/363,240A
             Sequence 615, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/363, ELLING DATE: December 23, 1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELES: 67-3510
INFORMATION FOR SEQ ID NO: 615
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                               Couture, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.

Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 tgttgga 7
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||5 TGTTGGA 9
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US-08-363-240A-616/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-08-363-240A-615
                                                                                   APPLICANT:
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                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INTORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: INDUCTION OF GRAPT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 631 West Fitch Street
                                                                                                                                                                                                     100.0%; Score 7; DB 2; L, 100.0%; Pred. No. 5.2e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTEN PARA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 05/000,951
FILING DATE: July 7, 1995
ATTORNEY AGENT INFORMATION:
NAME: MATDAIL SY RICHARY
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-585-684B-1366/C
; Sequence 1366, Application US/08585684B
; Patent No. 5877021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1366
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                     Query Match 100.

Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                             TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                               1 tgttgga 7
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US-08-585-684B-1366
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US-08-774-306A-246
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Pred. No. 5.2e+03;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: WIRUS REPLICATION
NUMBER OF SEQUENCES:
ADDRESSES:
ADDRESSES: 497
CORRESPONDENCES:
ADDRESSES: 497
CORRESPONDENCES:
ADDRESSES: 497
CORRESPONDENCES:
ADDRESSES: 497
CORRESPONDENCES:
ANDRESSES: 497
CORRESPONDENCES:
ANDRESSES: 497
CORRESPONDENCES:
ANDRESSES: 497
CORRESPONDENCES:
ADDRESSES: 497
CONTY: U.S.A.
ZIP: 90071-2066
COMPUTER: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPPRATING SYSTEM: IBM Compatible
OPPRATING SYSTEM: IBM Compatible
OPPRATING SYSTEM: BAC December 26, 1996
PRIOR APPLICATION NUMBER: US/08/774, 306A
FILING DATE: December 26, 1996
PRIOR APPLICATION NUMBER: 08/182,968
FILING DATE: May 14, 1992
ATTORNEY AGENT INFORMATION:
ANDER APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY AGENT INFORMATION:
ANDER APPLICATION NUMBER: 07/882,888
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: MAY 14, 1992
ATTORNEY,AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELEPHONE: (213) 955-0440
TELEPAX: (213) 955-0440
TELEPAX: (213) 955-0440
TELEPX: 67-3510
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleid acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 246, Application US/08774306A
Patent No. 5869253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 57.1%;
Matches 4; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : [::[f]
5 UGUUGGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-774-306A-246/C
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; Score 7; DB 2; Lk; Pred. No. 5.2e+03; 0; Mismatches 0;
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/585,684B FILING DATE: January 16, 1996
                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASISEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
633 West Fifth Street
Suite 4700
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Best Local Similarity 100.0
Matches 7; Conservative
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STRANDEDNESS: single
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STATE: California
COUNTRY: U.S.A.
                                                             CITY: Los Angeles
STATE: California
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                                                                                                                                 U.S.A.
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US-08-585-684B-1729
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Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; DB 2; Length 15; 100.0%; Pred. No. 5.2e+03;
                                                                                     Sequence 1367, Application US/08585684B

Patent No. 5877021

GENERAL INFORMATION:
APPLICANT: Strinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
TILLE OF INVENTION: METHOD AND REAGENT FOR THE
TILLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Saile 4700
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.0 Forget
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/1000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERRACE-DOCKET NUMBER: 32,818/07
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1367:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
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7; Conservative
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STRANDEDNESS: single
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STATE: California
COUNTRY: U.S.A.
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US-08-585-684B-1729/C
                                        RESULT 12
US-08-585-684B-1367/C
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Gaps
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Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: ADDRESS:
CORRESPONDENCE ADDRESS:
Length 15;
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Search completed: March 27, 2001, 08:19:22 Job time: 5149 sec
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APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 7; DB 2; L.
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 7; Conservative 0; Mismatches 0;
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MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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PELLING DATE: January 16, 1996

PROOR APPLICATION DATE:

APPLICATION NUMBER: 60/000,951

FILING DATE: JULY 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: WATUBLY, RICHARD

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELERA: 67-3510

INFORMATION FOR SEQ ID NO: 1731:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-585-684B-1731/c; Sequence 1731, Application US/08585684B; Patent No. 5877010; GENERAL INFORMATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-160
TELEPHONE: (213) 489-160
TELEPHONE: (213) 489-160
TELEPHONE: (713) 955-0440
ITELEX: 67-3310
INFORMATION FOR SEQ ID NO: 1730:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                218/078
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-585-6848-1730
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13 TGTTGGA 7
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100.0%; Score 7; DB 2; Length 15; 100.0%; Pred. No. 5.2e+03; ive 0; Mismatches 0; Indels
                                                                                           Query Match
Best Local Similarity 100.0
Matches 7; Conservative
; STRANDEDNESS: sir; TOPOLOGY: linear
US-08-585-684B-1731
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RSV 1C hammerhead RSV N hammerhead r RSV N hammerhead r Mouse relA hammerh Mouse relA hammerh Mouse relA hammerh	Human CD40 hammerh Human CD40 hammerh Human CD40 hammerh Human CD40 hammerh	Mouse CD40 hammerh Mouse CD40 hammerh Mouse CD40 hammerh Human B7-1 hammerh	Human B7-1 hammerh Human B7-1 hammerh Human B7-1 hammerh	Hz-1 Pagl gene dir	Transcript tag seq Tag sequence of a	HIV-1 protease gen HIV-1 protease gen Probe COD 1111 spe	1 mkNA rib fibroblas protease protease	HIV-1 protease gen HIV-1 protease gen HIV-1 protease gen HIV-1 protease gen HIV-1 protease gen					:y; therapy;						useful for, e.g mmunlty, and for	
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, c 13	c 19 c 20 c 21 c 22	0000	0000	c 30	nmn	nmm	1 w w 4 ⋅	0 0 0 4 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1	1D VS8899 XX XX V58899	7		XX Ceptospira XX VX W09840099-	17	00	(AGRI (PIGR			XX PS Claim
4.5 Compugen Ltd.	<pre>sarch time 207.51 Seconds (without alignments) 12.672 Million cell updates/sec</pre>				rs: 960044			seeqn/NA1980.DAT:* seeqn/NA1981.DAT:* seeqn/NA1982.DAT:*	sseqn/NA1984_DAT:* sseqn/NA1985_DAT:* sseqn/NA1985_DAT:*	sseqn/NA1987.DAT:* sseqn/NA1988.DAT:* neseqn/NA1989.DAT:*	neseqn/Nalyyu.DAT:* neseqn/Nalyy1.DAT:* neseqn/Nalyy2.DAT:*	neseqn/NA1993.DAT:* neseqn/NA1994.DAT:* neseqn/NA1995.DAT:*	geneseq/geneseqn/NA1996.DAT:* 'geneseq/geneseqn/NA1997.DAT:* 'geneseq/geneseqn/NA1998.DAT:*	Jacay geneseqy genesequivariants Jatay geneseqy geneseqn/NA2000 .DAT:* results predicted by chance to have a to the score of the result being printed, of the rotal score distribution		Description	င်များ		riv-1 protesse gen rb gene antisense HIV-1 protesse gen Neuroblastoma spec	RSV 1C hammerhead RSV 1C hammerhead
GenCore version pyright (c) 1993 - 2000 search, using sw model	ch 27, 2001, 08:22:59 ; Se	US-09-380-826A-5 7 1 tttgata 7	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	480022 segs, 187831343 residues	satisfying chosen parameter	h: 0 h: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	N_Geneseq_36:* 1: /cgn2_2/gcgdata/geneseq/genesegn/NA1980.DAT:* 2: /cgn2_2/gcgdata/geneseq/genesegn/NA1981.DAT:* 3: /cgn2_2/gcgdata/geneseg/genesegn/NA1981.DAT:* 4: /cgn2_2/gcgdata/geneseg/genesegn/NA1982.DAT:*	reyn.2.7/959aca/95neseq/95ne /cgn2_2/gcgdata/geneseq/95ne /cgn2_2/gcgdata/geneseq/9ene /cgn2_2/gcgdata/geneseq/9ene	/cgn2_2/gcgdata/geneseq/gene /cgn2_2/gcgdata/geneseq/gene /cgn2_2/gcgdata/geneseq/gen	/cgn2_2/gcgdata/geneseq/geneseqn/Nal991.DAT:*/cgn2_2/gcgdata/geneseq/geneseqn/Nal991.DAT:*/cgn2_2/gcgdata/geneseq/geneseqn/Nal992.DAT:*	/cgn2_2/gcgdata/geneseq/gen /cgn2_2/gcgdata/geneseq/gen /cgn2_2/gcgdata/geneseq/gen	/cgn2_2/gcgdata/geneseq/geneseqn/NA1996 /cgn2_2/gcgdata/geneseq/geneseqn/NA1997 /cgn2_2/gcgdata/geneseq/geneseqn/NN1998	2/gcgc 2/gcgc ber of r equal	SUMMARIES	y h Length DB ID	7 19 10 21 10 21	10 21	0 13 21 29/119 0 14 21 297691 0 15 14 052243	15 16 15 16
Co OM nucleic - nucleic	Run on: March	Title: US- Perfect score: 7 Sequence: 1 t	Scoring table: IDE Gap	hed:	Total number of hits	Minimum DB seq length: Maximum DB seq length:	Post-processing: Min Max Lis	Database : N_G 1: 2: 3 3:	 v		12:	14: 15: . 16:	17:	21: Pred. No. is t score greater and is derived		Result Query No. Score Match	7	4 2 9 c	c 9 7 100.0	~ ~

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  This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainel. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and diagnosis of past or present LS infection.
                                                                                                                                                                                                                                                                                                                                                                 SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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                                                                                                                                           100.0%; Score 7; DB 19; Length 7; 100.0%; Pred. No. 5.2e+07; tive 0; Mismatches 0; Indels
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                                                                                                            Sequence 7 BP; 2 A; 0 C; 1 G; 4 T; 0 other;
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98US-0090036.
98US-0090039.
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| tttgata 7
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Sequences 27573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding captressed in monocyte-derived dendritic cells compared differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while presentation of the cytotoxic immune response, particularly against tumour calls, immunostimal acrops factors play an important role in the cytotoxic immune response, particularly against tumour cells, immunostimalatory factors play an important role in the complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse complex) and subsequent recognition by T-cell receptors is alone insufficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses.

They may be used in vaccines to induce an immune response, particularly against a tumour antigen. to modulate the genotype of an APC; to screen for agents that modulate expression of discentially expressed genes in an APC; and as hybridisation probes/amplification primers for the expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in active immunotherapy (or to stimulate production of a presentation of endogenous APCs and uprequlates the APCs for the presentation of co-stimulatory signals, migration to Tcell-rich sites, correction of Tcell growth factors and uprequlates the APCs for the secretion of Tcell growth factors and uprequired for recruitment of immune effector cells.
                                                                                                                                                                                                                   Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer .
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98US-0111715.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                    Roberts BL, Shankara
                                         (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells). Issue (i.e. are upregulated in metastatic breast tumour cells). 203942 to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). Itsue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Or standard immunoassays or hybridisation/amplification reactions. Or second that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, or e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific cantibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antispen-specific immune effecter immune effecter immune effecter immune has a cells, immune has a superprediction and these used for adoptive
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Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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98US-0090039.
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98US-0090041.
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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                                                                                               Homo sapiens
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Co f e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic gentis disolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
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98US-0089997.
98US-0090039.
98US-0090040.
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                    Homo sapiens
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ò g Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens WO9965928-A2.

Metastatic breast tumour cell upregulated transcript tag #2351.

07-APR-2000 (first entry)

283117;

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Tablo 10 20234 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells). 283942 tepresent tags corresponding to distinct transcripts that are to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific continuousles (Ab). Ab are used to detect the polypeptides or as therapeutic agentic. Host cells that produce the polypeptides or as therapeutic agentic and isolate populations of educated, antigen-specific immune effecter immuncherancy.
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                                      Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
           Metastatic breast tumour cell upregulated transcript tag #2002.
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98US-0090039.
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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -

Shankara S;

Roberts BL,

WPI; 2000-106079/09.

98US-0089997. 98US-0090039. 98US-0090040. 98US-0090041.

19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998;

(GENZ) GENZYME CORP. ROBERTS B L.

(ROBE/) ROBERTS B L (SHAN/) SHANKARA S.

99WO-US13647. 98US-0089853

18-JUN-1999;

19-JUN-1998

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that are preferentially transcribed in the metastatic breast tumour trissue (i.e. are upregulated in metastatic breast tumour cells). 283942 to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). 283942 to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunosassy or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially computed that modulate expression of the transcripts are potentially the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also riboxymes or antisense sequences). The transcripts are also useful in vaccines. Polypetides encoded by the transcripts are also useful in vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypetides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immune effecter immune transcripts.
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Claim 1; Page 122; 219pp; English.
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Mismatches

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Query Match 100. Best Local Similarity 100. Matches 7; Conservative

RESULT

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us-09-380-826a-5.rng

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rb gene; antisense oligonucleotide; modulate; gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of drug-selected mutations in the HIV protease gene used to treat HIV infections
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                                                                                                                                                   Human immunodeficiency virus; HIV; protease; probe; detection; drug selected mutation; hybridisation; genotyping; infection; drug resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 7; DB 21; Length 13; Best Local Similarity 100.0%; Pred. No. 1.8e+04; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reliable detection of drug-selected mutation in HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 BP; 5 A; 1 C; 2 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rb gene antisense oligonucleotide rb-N-103
                                                                                                                     HIV-1 protease gene probe SEQ ID NO:209.
                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 37; 76pp; English.
297719/c
TD 297719 standard; DNA; 13 BP
                                                                                                                                                                                                                                                                                                                                                             98EP-0870143.
                                                                                                                                                                                                                                                                                                                           99WO-EP04317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V49155 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1998 (first entry)
                                                                                   26-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147219/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tttgata 7
                                                                                                                                                                                                                                                          WO9967428-A2.
                                                                                                                                                                                                                                                                                                                         22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                             24-JUN-1998;
                                                                                                                                                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                Stuyver L;
                                                   297719;
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V49155
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consecutive cytosines; do not contain two sequences of three consecutive mucleotides each able to form three H bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonocleotides are used to modulate expression of genes, particularly the genes for p53, ErB-2, junB, junD, TGF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or oligonocleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the rb gene. Of these, only oligonucleotides V49008-52 resulted in effective downregulation of negative growth control by rb, while oligonucleotides V49052-236 had little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V49008-236 represent antisense oligonucleotides directed against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of antisense oligo:nucleotide(s) which lack long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 7; DB 19; 1 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                        (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14 BP; 5 A; 1 C; 1 G; 7 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1 protease gene probe SEQ ID NO:181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Fig 9c; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Schlingensiepen K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )1/c
297691 standard; DNA; 14 BP.
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                                                                                                                                                                                                                                                                                     97EP-0101531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2000 (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-400910/35.
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25-NOV-1993.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the HIV protease gene. The method of detection allows the simultaneous characterisation of a range of codons involved in drug resistance using sets of probes optimised to function together in a reverse-hybridisation assay. 297517 to 297997 represent specifically claimed probes for use in the assay, and 297479 to 297501 represent specifically claimed HIV protease gene polymorphic nucleotide sequences. 297502 to 297515, and 297516 represent PGR primers for the HIV protease gene, and 297516 represents an HIV protease probe used in an example from the present invention. The method, probes and primers can be used for the detection of drug-selected mutations in the HIV protease gene. The method allows the simultaneous characterisation of a range of codons involved in drug resistance. The method may also be used for HIV protease genotyping assays. The probes are able to discriminate between
                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes the detection of drug-selected mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver; resistance; chemotherapeutic agent; colchicine; doxorubicin; colon; actinomycin D; vinblastine; small intestine; kidney; adrenal gland; adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia; human; chronic myelogenous leukemia; CML; follicular lymphoma; be-cell acute lymphocytic leukemia; acute lymphocytic leukemia; breall acute lymphocytic leukemia; breall acute lymphocytic leukemia; breall acute lymphocytic leukemia; perceir colon carcinoma; neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif; hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                          Detection of drug-selected mutations in the HIV protease gene used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The method allows rapid and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wild type and mutated protease sequences. The methor reliable detection of drug-selected mutation in HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; DB 21; I 100.0%; Pred. No. 1.8e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 37; 76pp; English.
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                                                                                                                                                                      98EP-0870143.
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                                                                                                                                                                                                               (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                 treat HIV infections
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Best Local Similarity
7; Conservē
                                                                                                                                                                                                                                                                                                  WPI; 2000-147219/13.
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                                        W09967428-A2
                                                                                                                           22-JUN-1999;
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                                                                                   29-DEC-1999
                                                                                                                                                                                                                                                         Stuyver L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     052243;
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The sequences given in Q51825-2266 represent areas of mRNAs which are associated with development or maintenance of chronic myelogenous leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or caute lymphocytic leukemia, for leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer. The full length mRNAs containing these target target caquences, encode aberant cellular proteins which are able to control cellular proliferation and are directly linked to a leukemic phenotype. These target sequences are identified by the ribozyme of the invention. The ribozymes is formed in a hammerhead motif, but may also be formed in the motif of a hairpin, hepatitis delta virus, group I intron or RNasepellke RNA. These ribozymes may be used to inhibit the development or expression of a transformed phenotype in man and content and also be corresponding expression of the corresponding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage of target mRNAs expressed in pre-neoplastic and transformed cells elicits inhibition of the transformed state. Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the mechanism of drug resistance used by transformed cells and thus enhances drug therapies for tumours. The ribozymes may also be used to study genetic drift and mutations within cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated with tumours or mRNA expressed from gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 14; Length 15; 42.9%; Pred. No. 1.8e+04; Live 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 10; 69pp; English.
                                                                                                        920S-093610
920S-0936421
920S-0936422
920S-0936531
920S-093632
920S-0987131
930S-0006122
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Conservative
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  93WO-US04573
                                                        32US-0882822
                                                                                   32US-0882885
                                                                                                                                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                 Draper KG, Thompson JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-386203/48.
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Best Local Similarity
Matches 3; Conserv
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13-MAY-1993;
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                                                                                                                                            1992;
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                                                                                                                                                                                                                               26-AUG-1992;
                                                                                                                                                                       26-AUG-1992)
26-AUG-1992)
                                                                                                                                                                                                                                                          07-DEC-1992;
                                                                                                                                                                                                                                                                                        19-JAN-1993
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                                                                                                                                            26-AUG-
                                                                                                                    26-AUG-
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Homo sapiens

WO9323057-A.

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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytial virus (RSV) at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the target sequences and can be used for treatment and diagnosis of
                                      atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rhemmatoid arthritis; psoriasis; myocardial ischbaemia; Kawassaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
  RSV; bcr-abl; oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dudycz LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz Li
Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J;
McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;
Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; onco translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 269; 407pp; English.
                                                                                                                                                                                                                                                                                                         94US-0228041.
94US-0245736.
94US-0291932.
94US-0291932.
94US-0291832.
94US-0292620.
94US-0303039.
94US-0311749.
94US-0311749.
94US-0311749.
94US-0311749.
94US-0311749.
94US-0311749.
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94US-0201109.
94US-0218934.
94US-0222795.
94US-0227958.
                                                                                                                     Respiratory Syncytial Virus
                                                                                                                                                                                                    95WO-IB00156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-) RIBOZYME PHARM INC.
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16-AUG-19
17-AUG-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SEP-1
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                                                                                            AIDS;
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Sequence 15 BP; 7 A; 0 C; 3 G; 5 U; 0 other;

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; artherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rhewmatoid arthritis; psoriasis; myocardial ischemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSV 1C hammerhead ribozyme target sequence (nt. position 17).
                            Length 15;
Score 7; DB 16; Length 15;
Pred. No. 1.8e+04;
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                          100.08;
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94US-0218934.
94US-0222795.
                                                  42.98;
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94US-0271280
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94US-0291433
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94US-0311486
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                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1997 (first entry)
Query Match
Best Local Similarity 42.5.
                                                                                                                                                                                                                                                                                                         T56962 standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0311
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16-AUG-1994;
17-AUG-1994;
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15-APR-1994;
15-APR-1994;
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29-MAR-1994;
04-APR-1994;
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RESULT 14
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                                                                                              The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytial virus (RSV) at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the target sequences and can be used for treatment and diagnosis of
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                         nzymes having modified bases and methods for producing them use in inhibiting disease related genes
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                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                               ; Score 7; DB 16; Length 15
Pred. No. 1.8e+04;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                 Sequence 15 BP; 7 A; 0 C; 3 G; 5 U; 0 other;
                                                                           Claim 2; Page 269; 407pp; English
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42.9%; E
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94US-0245736.
94US-0271280.
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94US-0218934
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                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 42.9
Matches 3; Conservative
                      WPI; 1995-351090/45.
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                                            Ribozymes
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  Woolf T;
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T56964
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytical virus (RSV) at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential harmerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM;
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Pred. No. 1.8e+04;
I; Mismatches 0;
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42.9%; F
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94US-0345516.
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94US-0316771.
94US-0319492.
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ID T57424 standard; RNA; 15 BP.
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94US-0293520
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les 3; Conserv
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Best Local S
Matches 3
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19-MAR-1997 (first entry)
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ID T57425 standard; RNA; 15
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13 TTTGATA 7
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transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                     Dudycz LW;
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Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J;
McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;
Sweedler D, Thompson JD, Tracz D, Usman N; Wincott FE;
Woolf T;
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illarity 100.0%; Pred. No. 1.8e+04;
Conservative 0: Mismatchhor
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                                                                                                                               9405-0201109.
9405-021109.
9405-0224795.
9405-0227958.
9405-0227958.
9405-0271280.
9405-0271280.
9405-0291932.
9405-0291433.
9405-0291433.
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94US-0311486.
94US-0311749.
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94US-0316771.
94US-0319492.
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94US-0334847.
94US-0337608.
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                                              Respiratory Syncytial Virus
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23-SEP-1
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19-AUG-1
                                                                                                                                                                                                             5-AUG-1
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                             AIDS;
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gene expression; downregulation; interleukin-5; IL-5; ICAN-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory synotial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroscierosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J; McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM; Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;
RSV N hammerhead ribozyme target sequence (nt. position 1148).
                                               Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0228041.
94US-0245736.
94US-0271280.
                                                                                                                                                                                                                                                                                                                                       Respiratory Syncytial Virus.
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94US-0319492
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94US-0224483
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94US-0345516
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94US-0363233
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94US-0334847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0311
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Woolf T;
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11-OCT-1994;
04-NOV-1994;
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23-DEC-1994;
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8-MAY-1994
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                                                                                                                                                                                                                                                                                       AIDS; ss.
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Gaps

; 0

Length 15; Indels

Query Match Best Local Similarity Matches 7; Conserv

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PT Ribozymes having modified bases and methods for producing them xx xx xx y S Claim 2: Page 276; 407pp; English.

XX XX XX Claim 2: Page 276; 407pp; English.

XX CC The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding CC for a protein of respiratory syncytial virus (RSV) at the corrected base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against that improve their nuclease resistance. The ribozymes cleave the traget sequences and can be used for treatment and diagnosis of XX Sequence 15 BP; 6 A; 4 C; 2 G; 3 U; 0 other;
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Gaps

.; 0

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Sequence 6, Appli
Sequence 7, Appli
                                                                                       March 27, 2001, 08:19:22 ; Search time 132.3 Seconds (without alignments) 8.527 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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                                                                                                                                                                                                                                                                                                            561672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS.COMS.seq:*
/cgn2_6/ptodata/2/ina/PcTUS.COMS.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-09-249-215-212
5-08-373-124A-90
5-08-291-932A-129
5-08-291-932A-130
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                                                                                                                                                                                                                                                                          280836 seqs, 80580151 residues
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                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
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length: 2000000000
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Match Length
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APP		
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sedneuce sed	System	0;
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2.23 2.23 2.23 2.23 2.23 2.24 2.24 2.25 2.20 2.20 2.20 2.20 2.20 2.20 2.20	a d A	1 1;
5-6848-2320 5-6848-2321 1-350-25 1-350-25 1-350-25 1-3124A-520 3-124A-1561 3-124A-2565 3-124A-2565 3-124A-2565 3-124A-2565 5-628-520 5-628-1561 5-628-1561	IGNMENTS sis of the et Bra/Brb Thereof 5.1 634	ore 7; DB ed. No. 7.] Mismatches
- 5 - 5 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6 - 6	ALIGNMENT 4 eh eb elet Bra/ ns Thereo on 5.1 6,634 83/132	Score 7 Pred. N Misma
US - 08 - 585 - 08 - 08 - 08 - 08 - 08 - 0	ALJ Saleh ar Bas ar Bas ar Bas rions rions rosion 7086,6	Scc Pre 0, N
000000000000000000000000000000000000000	US/08086634 US/08086634 Peter J. Sentot Saleh Wolecular Basis Human Platelet J 12 SS: A Lardner 1497 RM: Compatible PC-DOS/MS-DOS Fect, Version 5 DATA: US/08/086,634 MATION: UNERR: 30,383/13: RM: COMPATION: UNBER: 30383/13: TICS: A 128 NO: 6: TICS: d a airs d airs blie	100.08; 100.08; ive
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	334-6/C 6, Application 5. 5516634 INFORMAT: NEWANN, ISANT: SANTOSO, OF INVENTION: OF SEQUENCES: SECRET AND	Similar 7; Cons gata 7 [111]
		Match Local Simi les 7; 1 tttgata 7 TTTGATA
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Sequence Sequence Sequence

US-08-585-684B-2128 US-08-585-684B-2129 US-08-585-684B-2319

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Sequence Sequence

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Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Renneth G. Draper
APPLICANT: Bharat Chownira
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/166,664
FILING DATE:
CLASSIFICATION 435
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: US/07/884,074
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 197/062
REFERENCE/DOCKET NUMBER: 197/062
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    appplication
| below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICATION NUMBER: US/08/271,880A FILMS DATE: July 7, 1994
PRIOR APPLICATION DATA: Including apppl PRIOR APPLICATION DATA: described below APPLICATION NOMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/082,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 217, Application US/08271880A
; Patent No. 5693535
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street'
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-166-664-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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US-08-271-880A-217/c
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                                                                     Sequence 7, Application US/08086634

Patent No. 5516634

GENERAL INFORMATION:
APPLICANT: NEWMAN, Peter J.
TITLE OF INVENTION: Molecular Basis of the
TITLE OF INVENTION: Human Platelet Bra/Brb Alloantigen System and
TITLE OF INVENTION: Applications Thereof
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: P. O. Box 1497

CITY: Madison
STAFE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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Patent No. 5646020
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James A. McSwiggen
APPLICANT: J. Anthony Mamone
TITLE OF INVENTION: PREFERRED TARGETS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 1;
Pred. No. 7.1e+0
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ZIP: 53701-1497

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: WordPerfect, Version 5.1
CURRENT APPLICATION DATA:
FILLING DATE: 30-June-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INCURNALLY.
NAME: Scanlon, William J.
REGISTRATION NUMBER: 30,136
REFRENCE/DOCKET NUMBER: 3038:
TELECHONICATION INFORMATION:
TELEPHONE: (608) 258-4284
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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US-08-086-634-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-08-166-664-5/c
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                                         RESULT 2
US-08-086-634-7/c
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              James McSwiggen
Dan T. Stinchcomb
James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
HUMAN IMMUNOBERICIENCY VIRUS
                                                                                                                                                                    Length 13;
                                                                                                                                                                                                           0; Indels
                                                                                                                                                                  core 7; DB 2;
red. No. 7e+03;
Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
PRIOR APPLICATION NUMBER: 08/910,408
FILING DATE: AUR NOWN
APPLICATION NUMBER: 08/910,343
FILING DATE: AUGUST 6, 1993
APPLICATION NUMBER: 07/882,886
APTICATION NUMBER: 07/882,886
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 217: US-09-249-215-217
                                                                                                                                                                Query Match 100.0%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 217, Application US/09249215 Patent No. 6159692 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 217:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kenneth G. Draper
Bharat Chowrira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
  SEQUENCE CHARACTERISTICS
                                   TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-910-408-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-249-215-217/c
                                                                                                                                                                                                                                                   1 tttgata 7
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| Patent No. 5972704
| GENERAL INFORMATION:
| APPLICANT: Reneth G. Draper
| APPLICANT: Bharat Chowrira |
| APPLICANT: James McSwiggen |
| APPLICANT: James McSwiggen |
| APPLICANT: James McSwiggen |
| APPLICANT: James D. Thompson |
| TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS |
| TITLE OF INVENTION: REPLICATION |
| NUMBER OF SEQUENCES: 232 |
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 13; 7e+03;
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               0: Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/910,408
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,880
FILING DATE: July 7, 1994
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/682,886
FILING DATE: May 14, 1992
ATTORNICY DATE: MAY 16, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPÁTIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
                                                             206/116
                                                    REFERENCE/DOCKET NUMBER: 206. TELECOMMUNICATION INFORMATION: TELEFHONE: (213) 489-1600 TELETAX: (213) 955-0440 TELEX: 67-3510 INFORMATION FOR SEQ ID NO: 217: SEQUENCE CHARACTERISTICS: LENGTH: 13 base pairs TYPE: nucleic acid STRANBENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 217:
                   NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & L. STREET: 633 West Fis STREET: Sulte 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (213)
                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-271-880A-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 TTTGATA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 tttgata 7
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100.0%; Score 7; DB 2; Length 14; 100.0%; Pred. No. 7e+03; Ordels
                                                                                        APPLICANT: Kenneth G. Draper
APPLICANT: Bharat Chowrira
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: Dan T. Stinnthcomb
APPLICANT: James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
TITLE OF INVENTION: HUMAN IMMONOBERICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb medium TYPE: 3.5" Diskette, 1.44 Mb medium TYPE: Storage COMPUTER: IEM COMPATIBLE OPERATING SYSTEM: IEM P.C. DOS 5.0 SOFTWARE: FASTEM: Version 1.5 CURRENT APPLICATION DATA: US/08/910,408 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,880
FILING DATE: July 7, 1994
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WALDLEY, RICHARD
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 212, Application US/09249215

Patent No. 6159692

GENERAL INFORMATION:

APPLICANT: Kenneth G. Draper

Bharat Chowrira
                               Sequence 212, Application US/08910408
Patent No. 5972704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 206/
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                           GENERAL INFORMATION:
APPLICANT: Kennet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TTTGATA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tttgata 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-249-215-212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 90071
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                                             ;
0
                                               Gaps
                                             ;
0
                                                                                                                                                                                                                                               APPLICANT: Kenneth G. Draper
APPLICANT: Bharat Chowrina
APPLICANT: Bharat Chowrina
APPLICANT: Dan T. Stinchcomb
APPLICANT: James D. Thompson
APPLICANT: James D. Thompson
APPLICANT: James D. Thompson
TITLE OF INVENTION: HUMAN IMMUNDEFICIENCY VIRUS
TITLE OF INVENTION: HUMAN IMMUNDEFICIENCY VIRUS
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Sulte 4700
CITY: Los Angeles
STRATE: Califor Angeles
COMPTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 7; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 7e+03; Matches 7; Conservative 0; Mismatches 0; Indels
  Length 13;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM IFE: SLUTBYE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTESD Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,880A
FILING DATE: July 7, 1994
PRIOR APPLICATION DATA: including appplication
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 04/103,243
FILING DATE: May 14, 1992
APTORNEY/AGENT INFORMATION:
NAME: Way 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Way BICHARD
REGISTRATION NUMBER: 32,327
      core 7; DB 3; Ired. No. 7e+03; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
      100.0%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                        Sequence 212, Application US/08271880A
Patent No. 5693535
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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3 TTTGATA 9
                                                                                                                      10 TTTGATA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-271-880A-212
                                                                                             1 tttgata 7
                                                                                                                                                                                                                             US-08-271-880A-212
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Gaps ;

James McSwiggen Dan T. Stinchcomb

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us-09-380-826a-5.rni

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APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: BLAZES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NP-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.6" DISKETE, 1.44 Mb
MEDIUM TYPE: 1BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFFWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: FEBRUARY 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: May 18, 1892
APPLICATION NUMBER: 07/987,132
FILING DATE: May 18, 1892
APPLICATION NUMBER: 07/936,422
ATTORNEY,AGENT INFORMATION:
NAME: WALDLIG, RICHARD
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 7; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 129, Application US/08291932A Patent No. 5658780 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,327
ER: 209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (213) 499-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTR: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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11 TTTGATA 5
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                                                                                      90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-373-124A-90
                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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0
James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
HUMAN IMMUNOBELICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 7; DB 3; Length 14; 100.0%; Pred. No. 7e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICENT NO. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: MACSAIgen, James
APPLICANT: MACSAIgen, James
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION DATE:

RELING DATE: CURNOWN
APPLICATION NUMBER: 08/910,408
FILING DATE: August 6, 1993
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REFERENCE/DGCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 212: US-09-249-215-212
                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-373-124A-90/c
; Sequence 90, Application US/08373124A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 212:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                            NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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Best Local Similarity 100.
Matches 7; Conservative
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3 TTTGATA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCSwiggen, James
MCSWIGGEN RIBOZYME TREATMENT OF
VVENTION: DISEASES OR CONDITIONS
VVENTION: RELATED TO LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 131, Application US/08291932A patent No. 5658780 GENERAL INFORMATION:
                                                                                                                                                208/157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
                     FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
    08/245,466
                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REDECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: (67-3510
TELEX: (7-3510
TELEX: (7-3510
TELEX: (7-3510
TELEX: (7-3510
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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42.9%; F
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REGISTRATION NUMBER: 32
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TITLE OF INVENTION: DIST
TITLE OF INVENTION: RELA
TITLE OF INVENTION: NF-14
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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STATE: California
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              linear
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7 UUUGAUA 13
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US-08-291-932A-130
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                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: APPLICATION APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 7e+(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IDM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7;
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SOFTWARE: Word FC. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
APPLICATION NUMBER: US/08/291,932A
APPLICATION NUMBER: US/08/291,932A
OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A FILING DATE: August 15, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-291-932A-130
Sequence 130, Application US/08291932A
Patent No. 5558780
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/COCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Lyon & Lyon
633 West Fifth Street
Suite 4700
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TITLE OF INVENTION: RELATED
TITLE OF INVENTION: RELATED
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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Best Local Similarity
Matches 3; Conserv
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90071-2066
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9 UUUGAUA 15
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                                                                        Indels
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Pred. No. 7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING RESPIRATORY TITLE OF INVENTION: SYNCYTIAL VIRUS CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 90071-2066
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Mord Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 5693532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
RILING DATE: NO. 5693532ember 4, 1994
APPLICATION NUMBER:
APPLICATION NUMBER:
RILING DATE:
APPLICATION NUMBER:
APP
                                                                        Mismatches
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGIESTRATTON NUMBER: 32,327
REERENDCE/DOCKET NUMBER: 209/TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELER: (7-3510
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                            ; Sequence 9, Application US/08334847
; Patent No. 5693532
                                                                        4 ;
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.98;
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Best Local Similarity 42.9.
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                                                                     .3; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
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6 UUUGAUA 12
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US-08-334-847-9
                                                                     Matches
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Pred. No. 7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08334847
Patent No. 5693532
GENERAL INFORMATION: APPLICANT: MCSWiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.00
COMPUTER: 1BM Compatible
COMPUTER: 1BM P.C. DOS 5.0
CUSTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FTLING DATE: NO. 5693532ember 4, 1994
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
LELEFAX: (213) 489-1600
LELEX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 131:
SEQUENCH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
7-291-932A-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
42.9%; F
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TELEFAX: (213) 955-0440
TELEX: 67.3510
INFORMATION FOR SEC ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 42.9
Matches 3; Conservative
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STRANDEDNESS: single
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Best Local Similarity
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6 UUUGAUA 12
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US-08-291-932A-131
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US-08-334-847-8
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gb_est73:*
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  (without alignments)
  19.482 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                           OM nucleic - nucleic search, using sw model
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A2323820 1M0045A01
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1M0045A01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0045A01 R, DNA sequence.
AZ323820
AZ323820.1 GI:10378917
GSS.
house mouse.
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AA226145 nc09f09.r
AA846437 a185c09.s
                                                                           pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                    Description
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AZ402088
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase are Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qib|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
T=1: 801 585 5177
Email: ddunn@genetics.utah.edu
                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn,D., Aoyadi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1M0342C04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0342C04 R, DNA sequence.
AZ502952
AZ502952.1 GI:10684268
                                    Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-" /note="Vector: PWHQ2Nv; Puiffied genomic DNA from M. musculus G57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 10000 Std Error: C
Plate: 0053 row: C column: 07
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0053C07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 22.
Location/Qualifiers
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Best Local Similarity 100.0
Matches 7; Conservative
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AZ502952/c
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                                                                                                                                                                                                                                            plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Jalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/61 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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11 TTTGATA 5
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AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwn42 (qi|4732114|qplhAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptors and selected for amplicially into statement of (Stratagene) cells and selected for amplicially resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Mr. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Buanyota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 7; Conservative 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: P column: 11
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High quality sequence stop: 23.
Location/Qualifiers
AZ345476.1 GI:10424713
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Fax: 801 585 7177
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                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn,D., Aoyagi,B., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/dboxref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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100.0%; Score 7; DB 173; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0342 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
                                                                                                     Mus musculus
                                                                   house mouse.
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb.
Plasmid Inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacres,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Lenath: 10000 Std Error: 0.00
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Plate: 0134 row: M column: 14
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil47321H qiplARL29072.1), a copyrnumber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Mus musculus

Bukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Slam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
/lab.host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \mbox{Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 7; DB 173; Length 24; Best Local Similarity 100.0%; Pred. No. 2.2e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: P column: 17
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                             plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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SOURCE

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

DEFINITION

ACCESSION VERSION KEYWORDS

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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: L column: 20
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                           /sex="Male"
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Fax: 606 257 1717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4896"
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/clone="spc04231"
/clone="penfine"schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="vector: M13mp19; The cDNA library of
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Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ404619 25 bp DNA GSS 03-OCT-2000 1M0173L20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0173L20 F, DNA sequence.
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                                                                                                                                               Schizosaccharomyces pombe
Eukaryota; Fungi: Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.

1 (bases 1 to 25)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
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         AU008929 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc04231, mRNA sequence.
                                                                                                                                                                                                                                                                                                               Unpublished (1998)
Contact: Mitsuoki Morimyo
Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
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    25
    /organism="Schizosaccharomyces pombe"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                 AU008929.1 GI:3345387
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Fax: 801 585 7177
                                                                                                                                  fission yeast.
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11 TTTGATA 5
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84112,
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BASE COUNT ORIGIN

DEFINITION

RESULT AZ404619

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

source

FEATURES

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114) gblAPL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored for amplicitlin resistance."
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Smullan, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                      /lab host="E. Coll strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pneumocystis carinii f. sp. carinii.
Pneumocystis carinii f. sp. carinii
Eukaryota; Fungi; Fungi incertae sedis; Pneumocystidaceae;
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/strain="c57BL/6J"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gblAF129072.1). a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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1M0065E13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0065E13 R, DNA sequence.
                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Longarcre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="UUGC1M0052D24"
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                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
Fal: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: D column: 24
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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  AZ328549.1 GI:10388388
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                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 27)
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Unpublished (2000)
                                                                             Mus musculus
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                                                                     /clone_lib="AGS-1"
/lab_host="E. col;"
/lab_host="E. col;"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZAI0e9" from a single rat (99-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"
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/strain="C57BL/6J"
/db_xref="taxon:10092"
/clone="md2066"
/clone_lib="Mouse 3'-directed"
/tissue_ltype="decidual tissue (day 6.5-8.5 of gestation)"
/ d c d g b t
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Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K. Analysis of gene expression in mouse embryogenesis by 3'-directed cona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D18735 27 bp mRNA EST 12-DEC-1995 MUSGS01797 Mouse 3'-directed Mus musculus domesticus cDNA clone md2066 3', mRNA sequence.
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                        /organism="Pneumocystis carinii f. sp. carinii"
/db_xref="taxon:38081"
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Pred. No. 2.2e+05;
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3-1 Yamada-oka, Suita, Osaka 565, Japan.
Location/Qualifiers
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Mus musculus domesticus
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/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321141gb]AR129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Weissity of Utah
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                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/sex-"Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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/clone="UUGC1M0065E13"
                                                                                      Mus musculus
Eukaryota: Metazoa; Chordata;
Mammalia: Eutheria; Rodentia;
1 (bases 1 to 27)
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AZ335603
AZ335603.1 GI:10404082
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Fax: 801 585 7177
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                                                                   house mouse.
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/organism="Schizosaccharomyces pombe"
/strain="97"
/db_xref="taxon:4896"
/clone="spc02033"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 30)
1 (bases 1 to 30)
2 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (3301) 496-1550
Email: Robert_Strausberg@hih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMM128 row: f column: 19
High quality sequence stop: 30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 30) Morimyo,M. and Mita,K. Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Location/Qualifiers
Schizosaccharomyces pombe cDNA clone spc02033, mRNA sequence.
AU007442
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                                                                                                                                                                                                                                                                        fission yeast.
Schizosaccharomyces pombe
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/db_xref="Laxon:10000"
/clone="InAGE:3967130"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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Tel: 06-877-5111(ex.3315)
Email: Kousaku@incb.osaka-u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not
Submitting the same cDNA sequence redundantly to DDBJ since 1993.
For the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see '
http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
represented by this GS sequences is also found there.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 30)
6 Notubo, K.
BodyMap; human gene expression database
Unpublished (1995)
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HUMGS0004973 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
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/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
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Institute for Molecular and Cellular Biol
Osaka University
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  Location/Qualifiers
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C20899
C20899.1 GI:1622009
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Matches 7; Conservative
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Search completed: March 27, 2001, 07:38:23 Job time: 4586 sec

Run on:

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U52077 Human marin
U60994 Leptospira
U66913 Dictyostell
X89236 S.pyogenes
A48819 Sequence 13
A48820 Sequence 14
Z49321 S.cerevisla
A45813 Sequence 7
A45814 Sequence 8
Z49320 S.cerevisla
U36757 Mus musculu
AC014767 Drosophil
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M95263 Human chrom
G50458 SHGC-79916
D38547 Small round
AJ009225 Bos tauru
AJ009224 Bos tauru
AJ009223 Bos tauru
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AP000145 Homo sapi
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PCR components: 25 ng of human genomic DNA, 10 pmol of each oligonucleotide, 200 micro-M dNTPs, 0.25 U raq polymerase (Cetus) oligonucleotide, 200 micro-M dNTPs, 0.25 U raq polymerase (Cetus) in 10 micro-l of 50 mM KCl-20 mM Tris-HCl, pH 8.3 (at room temp). 2.5 mM MgCl-2. Initial denaturation at 94degC for 1.5 min, then 30 eycles of 94degC for 15 sec, 62degC for 23 sec, and 72degC for 30 sec, followed by a final extension at 72degC for 3.5 min, using a perkin-Elmer 9600 thermocycler. PCR-amplified product size 279 bp. Sequence submitted by:
                                                                                                                   M95263.1 GI:177262
M95263.1 GI:177262
STS; human chromosome 4; sequence tagged site.
STS; human chromosome 4; sequence tagged site.
STS; human chromosome 4 toomid library, plate 4-1-2R, pos3C; vector SuperCos 1
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)

200010, R.D., dislibto, G., Xu, H., Lang, D.B., Dadgar, J., Magrane, G., Dugaiczyk, A., Smith, K.A., Cox, D.R., Masters, S.B. and Myers, R.M. The development of sequence-tagged sites for human chromosome 4 hum. Mol. Genet. 2 (8), 1271-1288 (1993)
                                                                        HUM4STS161 435 bp DNA STS 26-FEB-1996
Human chromosome 4 sequence-tagged site STS4-161, sequence tagged
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G50458 668 bp DNA STS 30-MAR-2000
SHGC-79916 Human Homo sapiens STS genomic, sequence tagged site.
G50458
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63.6%; Pred. No. 1.2e+03;
...matches 8; Indels
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University of California San Francisco
San Francisco, CA 9443-0925 USA
Phone: (415) 502-1612 Fax: (415) 476-8391
e-mail: hgmcprobes@cgl.ucsf.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 668)
Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
Unpublished (2000)
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/db_xref="taxon:9606"
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316..340
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92 TGTTGGAAGCTACCTTTTGATA 113
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                                         Z7845 Caenorhabdi
AF644659 Caenorhabdi
U07562 Human ABL q
AC026482 Homo sapi
AC084757 Homo sapi
AC083757 Homo sapi
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AC08839 Homo sapi
AC016064 Homo sapi
AC016064 Homo sapi
AC01315 Homo sapi
AC021315 Homo sapi
AC025178 Homo sapi
AC025978 Homo sapi
AC086408 Homo sapi
AC086408 Homo sapi
AC0867 Homo sapi
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AC08667 Homo sapi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-MAR-1998) Biochemistry and Molecular Biology, Uniformed Services University of the Health Sciences, 4301 Jones Bridge Road, Bethesda, MD 20814-4799, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-1999
5' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%; Score 14; DB 53; Length 239; 63.6%; Pred. No. 1.3e+03; ...ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the human hepatic squalene synthase
J. Biol. Chem. 268 (17), 12818-12824 (1993)
93286128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="squalene synthase"
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Guan, G., Dai, P.H. and Shechter, I.
Direct Submission

    .239
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /chromosome="8"

                                                                                                                                                                                                                              AC021315
HS225D2
AC008408
                                                                                                                      AF271897
AC083757
AE002828
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AC016064
AC014851
AC036189
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AF285442
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                                                                                                                                                                                                                                                                                                                                        AC008967
AC011438
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                                              CEM03B6
 AE002102
                                                                            CEC34B4
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33. .>239
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Matches 14; Conservative
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/translation="MAQAIIGAIAASAAGSALGAGIQAGAEAALQAQRYQQDLTLQQN
SFNIDKEMLGYQMENKLLAKNLNTRYSLLQAGGISSSDAARAVAGAPVTRLVDWGG
YRAAPQSSATTLRSGNFMAVDLPAQPKQKPLASEGYSNPAYDPVQRTASWVGSQNSS
RSWGPYHRQALQTVWYTPFGSSSVGTAPRGYFNTDRLPLFANLRR"
251 c 233 g 302 t
                                                                                                                                                                 /isolate="patient; SRSV-CHIBA-407/87/J"
Ad_xref="taxon:37141"
//note="SRSVs are currently recognised as a potential human calicivirus."
                                                                                                                                                                                                                                                                                                                                     /translation="VPCLLPQEYITHFISEQAPIQGEAALLHYVDPDTNRNLGEFKLY
PGGYLTCVPNSSSTGPQQLPLDGVFVFASWVSRFYQLKPVGTAGPARGRLGVRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Direct Submission

Submitted (04-UNN-1998) Bigot Y., Institut de Recherche sur la Biologie de l'Insects, UPRESA CNRS 6035, Facult des Sciences, Parc Grandmont, 37200 Tours, FRANCE

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1257)
Demattei, M.V., Auge-Gouillou, C., Pollet, N., Meunier-Rotival, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 2 (bases 1 to 1015)
Utagawa, E.T., Takeda, N., Inouye, S., Kasuga, K. and Yamazaki, S.
3'-terminal sequence of a small round structured virus (SRSV) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Features of the mammal marl transposons in the human, sheep, cow and mouse genomes and implications for their evolution
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AJ009225
AJ009225.1 GI:9187451
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Pred. No. 1.1e+03;
0; Mismatches 8; Indels
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                                                                         Arch. Virol. 135 (1-2), 185-192 (1994)
94256839
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                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAA07550.1"
/db_xref="GI:1232113"
                                                                                                                                                                                                                                                                                                /protein_id="BAA07549.1"
/db_xref="G1:1232112"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transposon="Hsmar1"
/db_xref="taxon:9913"
/clone="btmlec4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%;
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Direct Submission
Submitted (17-OCT-1994) to the DDBJ/EMBL/GenBank databases. Etsuko
T. Utagawa, National Institute of Health; 1-23-1 Toyama,
Shinjuku-ku, Tokyo 162, Japan (Tel:03-5285-1111(ex.2562),
Fax:03-5285-1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC ends sequenced at TIGR from the RPC111 BAC library. Designed and developed at the Stanford Human Genome Center. Location/Qualifiers
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                                                                                                                                                                                  95 degrees C for 10 minutes
94 degrees C for 30 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
Perkin Elmer 9700
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Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 668;
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each 1 uM
each 200 uM
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small round structured virus
Viruses; ssRNA positive-strand viruses, no
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Pred. No. 1.2e+03;
0; Mismatches 8;
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                                  4005 Miranda Ave. 2nd Fl., Palo Altc
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@bhgc.stanford.edu
Primer A: GCACATTAGCTCTTGGATTGCTT
Primer B: TGCCTTGTGGTTTAGCAATTTTT
STS size: 278
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                         AmpliTaq Gold Polymerase:
Total Vol:
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50 mM
10 mM
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31. 53
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PCR Cycles:
Thermal Cycler:
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primer_bind
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Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la Biologie de l'Insects, UPRESA CNRS 6035, Facult des Sciences, Parc Grandmont, 37200 Tours, FRANCE Location/Qualifiers
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Bigot,Y.

Direct Submission
Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la Submitted (04-JUN-1998) Bigot Y., Institut des Sciences, Parc Biologie de 1/Insects, UPRESA CNRS 6035, Facult des Sciences, Parc Grandmont, 37200 Tours, FRANCE
Grandmont, 37200 Tours, FRANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BTAJ9223 1276 bp DNA MAM 11-JUL-200
Bos taurus mariner related transposon Hsmarl, clone btmlec2.
AJ009223
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                                                                                                                                                                                                                                                                                Length 1258;
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Pred. No. 1.16+03;
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Pred. No. 1.1e+03;
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/db_xref="taxon:9913"
/clone="btmlec2"
1 261 c 248 g
                                                                                                          1. .1258
/organism="Bos taurus"
                                                                                                                                                   /transposon="Hsmarl"
/db_xref="taxon:9913"
/clone="btmlec3"
262 c 266 9
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transposon.
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Best Local Similarity 63.6%;
Matches 14; Conservative
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Best Local Similarity 63.6
Matches 14; Conservative
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Bos taurus
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Demattei, M. V., Auge-Gouillou, C., Pollet, N., Meunier-Rotival, M. and
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Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la
Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la
Biologie de l'Insects, UPRESA CNRS 6035, Facult des Sciences, Parc
Grandmont, 37-200 Tours, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus.
Bos taurus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                               Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
M (Dases 1 to 1257)
Demattei, M.V., Auge-Gouillou, C., Pollet, N., Meunier-Rotival, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Features of the mammal marl transposons in the human, sheep, cow and mouse genomes and implications for their evolution Mamm. Genome In press 2 (bases 1 to 1258)
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Bos taurus mariner related transposon Hsmarl, clone btmlec3.
AJ009224
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Homo sapiens mariner related transposon Hsmarl, clone mlehsc3.
AJ009229
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Pred. No. 1.1e+03;
0; Mismatches 8; Indels
                                                                    63.6%; Score 14; DB 3; Length 12f
63.6%; Pred. No. 1.1e+03;
ive 0; Mismatches 8; Indels
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/db_xref="taxon:9606"
/clone="mlehsc3"
263 c 264 9
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Best Local Similarity 63.6%;
Matches 14; Conservative (
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Best Local Similarity 63.6
Matches 14; Conservative
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/traislation="MSTRPSEIDLKKSSEVNNDSINNDNNNSINNDNNNNGNNKEE
TSEYTDPNNIFNKFRKLSSDKSFYKWFLQVGSNNNNBQTDSNTISNLSFYIATORIKN
ISBULTKKSYKSNSSELSOINGYGGAEIYIFRCLUDSIDFKNTNFPITTSPTTASA
TSTTTSTPTTPSTTASSTAASSSSSNOLKIOLFKOBFSKLTKQPHFISVLCKRFDGYE
VLNNFFLVHFSSTLKLTPSHEIMLGLALSGSLDKEVREQADKFLLNTLIQLSGSNTKS
Submitted (12-JUN-1996) Microbiology, Monash University, Wellington Rd., Clayton, VIC 3168, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSNNNNNNTTNIPDEWNISIFVDVIKELYPTIDWDIVIREMDCPIVNNMDQRGLAFI
LAVYKKATQVDQQQSKPFPIDFILDRVWVNSLSQIQFLKIAIQSDFFPFQNSTKKRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (15-AUG-1996) Dept. of Biology 0322, University of
California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="site of plasmid insertion in mutant organisms; mutants form crinkled, branching fingers; neither spores nor stalk cells were seen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDU66913 2321 bp DNA INV 05-SEP-1996
Dictyostelium discoideum ORF DG1040 gene, partial cds.
U66913
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/note="ORF DG1040; initially derived from a plasmid
                                                                                                                                                                                                                                                               Length 1481;
                                                                                                                                                                                   2 others
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/strain="AX4"
                                                                                                                                                                                                                                                 Score 14; DB 2; Len
Pred. No. 1.1e+03;
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Dictyostellum discoideum
Dictyostellum discoideum
Ekaryota, Dictyostellida, Dictyostellum.
1 (bases 1 to 2321)
Loomis, W.F.
                                                                            /organism="Leptospira fainei"
/strain="Hurstbridge"
/db_xref="taxon:48782"
<1. ->1481
/product="168 ribosomal RNA"
a 335 c 439 g 314 t
                                                                                  fainei"
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/cell_line="AX4"
join(370. .732,813. .>2321)
/note="ORF DG1040"
                                                                                                                                                                                                                                                                                                          0; Mismatches
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/db_xref="G1:1519538"
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Matches 14; Conservative
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YDNRRRPAQWLDREEAPKHFPKPNLHQKKVMVTVWWSAAGLIHYSFLNPGETITSEKY
AQOIDEWHRKLQRLQPALVNRKGPILLHDNARPHVAQPFLQKLNELGYEVLPHPPYSP
DLSPTDYHFFKHLDNFLQGKRFHNQQDAENAFQEFVESRSTDFYATGINKLISRWQKC
VDCNGSYPD**
1256. .1287
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VQWWFKKFCKGDESLEDEERSGRPSEVDNDQLRAIIEADPLTTTREVAEELNVDHSTV
                                                                                                                                                                           Gene 1203 (1997)

98121293 (1997)

2 (bases 1 to 1287)

Robertson, H.M.

Bolirect Submission

Submitsion (11-MAR-1996) Hugh M. Robertson, Entomology, University of Illinois at Urbana-Champaign, 505 S. Goodwin, Urbana, 1L 61801.
                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidạe; Homo.
                                                                                        1 (bases 1 to 1287)
Robertson, H.M. and Zumpano, K.L.
Molecular evolution of an ancient mariner transposon, Hsmarl, in the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="consensus sequence based on 20 unique sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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1 (bases i to 1481)

Perolat, P., Chappel, R.J., Adler, B., Baranton, G., Bulach, D.M., Billinghurst, M.L., Letocart, M., Merien, F. and Serrano, M.S. Leptospira fainei sp. nov., isolated from pigs in Australia Int. J. Syst. Bacteriol. 48 Pt 3, 851-858 (1998)
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Adler,B., Chappel,R.J., Baranton,G., Bulach,D.M.,
Billinghurst,M.L., Letocart,M., Merien,F., Serrano,M.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFU60594 1481 bp DNA BCT 10-SEP-19
Leptospira fainei 16S ribosomal RNA gene, partial sequence.
U60594
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Pred. No. 1.1e+03;
0; Mismatches 8;
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/protein_id="AAC52010.1"
/db_xref="GI:1263081"
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/transposon="Hsmarl"
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284 c 278 g
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179. .1210
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Submitted (29-JUN-1995) A. Podbielski, Institut f Med
Mikrobiologie, an der Rhein Westf. Techn. Hochschule, Aachen,
Pauwelsstr Klinkum, 52057 Aachen, FRG
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groEL gene; heat shock protein 60 (GroEL) like protein.
Streptococcus pyogenes.
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Pred. No. 1e+03;
0; Mismatches 8; Indels (
                                Length 2321;
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Pohl,B., Podbielski,A. and Zarges,I.
Unpublished
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/db_xref="G1:2462692"
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Location/Qualifiers
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/isolate="CS101"
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Pred. No. 1e+03;
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Deblacer, R.Y., Desomer, J. and Dhaese, P.
PERESSION OF SURFACE LAYER PROTEINS
PATENT: WO 9519371-A 14 20-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deblaere, R. Y., Desomer, J. and Dhaese, P. EXPRESSION OF SURFACE LAYER PROTEINS Patent: WO 9519371-A 13 20-JUL-1995; SOLANX (BE)
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Sequence 14 from Patent W09519371.
A45820 GI:2300193
A45819 3666 bp DNA
Seguence 13 from Patent W09519371.
A45819
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/organism="unidentified"
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/organism="unidentified"
/db_xref="taxon:32644"
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GTLTVTYADAKNAAGVAENITASVTLKKTTGAITSDTFTQGVLPSAATAAEYTSKSIA
ADYTFATGEGFTLNIDNAGAQVINLAGKKGAQGVADAINATFAGTATVSGDKVVIKSA
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TTAVAFGTAPTANTFVSAANTLASVADQAANLAATIDTLNTADKFTASATGATITT
STVTPVGTTITEPVITLK"
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MMLSNWALSPRYVGQRNLIHCTTLFHTLTRWAKDADDKYHDINSMYENMFTPSNDNVS
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IQSLSTSPYYNLALENYVFKNTPRAKRGPDNCRLLFYINDRCAVIGKNQNLWQEVDLA
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SSGVHSVKSKIKNVGIITPNQFIAVVSERFQKTFKVDGEIPIYYCDEFKSINDEIKDA
MNTLQSEQWKYFSGPKFSVKIKDKGLTIKVEKGMIYDCDRNDLIGLEFKGFLENIDSY
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Bukaryota; Fungil, Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 3915)
Unpublished
Unpublished
2 (bases 1 to 3915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-SEP-1995) Data collected by MIPS on behalf of the European yeast chromosome X sequencing project. MIPS at the Max-Planck Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG: E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                            Gaps
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complement(2736. 3067)
/note="solo delta"
3266. 3337
/gene="tR(TCT)JL2 - systematic name"
3266. 3337
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Pred. No. 1e+03;
0; Mismatches 8; Indels
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S.cerevisiae chromosome X reading frame ORF YJL046w.
249321 X13136
249321.1 GI:1008176
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/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
152. .1507
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/gene="tY(GTA)JL - systematic name"
complement(2445. .2735)
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/db_xref="GI:1008177"
/db_xref="SWISS-PROT:P47051"
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Best Local Similarity 63.69
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AUTHORS
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/gene="tR(TCT)JL2 - systematic name"
3348. .3419
/gene="tD(GTC)JL2 - systematic name"
/note="tD(GTC)JL2 - systematic name;
3348. .3419
/gene="tD(GTC)JL2 - systematic name"
a 667 c 698 g 1292 t
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13 59.1 2190 20 13 59.1 2508 18 13 59.1 3519 21 13 59.1 3519 21	13 59.1 4012 18 13 59.1 5253 21	13 59.1 10723 18 13 59.1 10723 18 13 59.1 10723 18 13 59.1 11802 18	13 59.1 1230025 20 13 59.1 1664976 19 12.4 56.4 30 21	12.4 56.4 30 21 12.4 56.4 200 19 12.4 56.4 300 20	12.4 56.4 310 20	12.4 56.4 706 20	12.4 56.4 877 18 12.4 56.4 977 18 12.4 56.4 915 19 12.4 56.1 062 21	12.4 56.4 1034 18 12.4 56.4 1034 18 12.4 56.4 1131 18 12.4 56.4 1152 18	41 12.4 50.4 1248 21 A05803 42 12.4 56.4 1249 19 X14031 43 12.4 56.4 1322 20 X13419 44 12.4 56.4 1353 18 X30790 45 12.4 56.4 1356 19 V04491	ALIGNMENTS		SULT 1 8901	V58901 standard; DNA; 22 BP.	V58901;	20-JAN-1999 (first entry)	eptospira	nfection; pathogenic Leptospira; iagnosis; ss.	0 0	17-SEP-1998.	06-MAR-1998; 98WO-AU00145.	07-MAR-1997; 97AU-0005494.	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD. (PIGR-) PIG RES & DEV CORP.	Chappel RJ;	WPI; 1998-520791/44.	New isolated pathogenic Leptospira bacterium - useful for, e developing products for conferring protective immunity, and prophylactic or therapeutic treatment	Claim 15; Page 72; 94pp; English.
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on 4.5 0 Compugen Ltd.		<pre>; Search time 207.51 Seconds (without alignments) 39.827 Million cell updates/sec.</pre>	22		residues	ameters: . 960044		W	N_Geneseq_36:* 1: /cgn2_2/gcgdata/geneseg/geneseqn/NA1980.DAT:* 2: /cgn2_2/gcgdata/geneseg/geneseqn/NA1981.DAT:* 3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*	q/geneseqn/NA1983.DAT:* q/geneseqn/NA1984.DAT:* q/geneseqn/NA1985.DAT:*	q/geneseqn/NA1986.DAT:* q/geneseqn/NA1987.DAT:*	q/geneseqn/NA1988.DAT:* eq/geneseqn/NA1989.DAT:*	eq/genesegn/NA1990.DAT:* eq/genesegn/NA1991.DAT:*	eq/geneseqn/NA1992.DAT:* eq/qeneseqn/NA1993.DAT:*	gogdata/geneseq/genesegn/NA1994.DAT:* //ccddata/geneseg/genesegn/NA1995.DAT:*	/genesegn/NA1996	/geneseqn/NA1998 /geneseqn/NA1999 /geneseqn/NA1999	ipredicted by chance to have a score of the result being printed, total score distribution.	IES		Description	□ □	Leptospira nucleor Nucleic acid seque T fainsi mudlasti	A encodi	encodir n gene	Nucleotide sequenc MAP Kinase #2 codi
GenCore version Copyright (c) 1993 - 2000	eic search, using sw model	08:22:59	US-09-380-826A-6 22 1 tgttggannnnnntttgata	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	480022 segs, 187831343 re	hits satisfying chosen parameters	length: 0 length: 200000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	N_Geneseq_36:* 1: /cgn2_2/gcgdata/genese 2: /cgn2_2/gcgdata/genese 3: /cgn2_2/gcgdata/genese	<pre>. /cgn2_2/gcgdata/genese . /cgn2_2/gcgdata/genese . /cgn2_2/gcgdata/genese</pre>	<pre>: /cgn2_2/gcgdata/genese : /cgn2_2/gcgdata/genese</pre>	: /cgn2_2/gcgdata/genese 0: /cgn2_2/qcqdata/genes	<pre>1: /cgn2_2/gcgdata/genes 2: /cgn2_2/gcgdata/genes</pre>	3: /cgn2_2/gcgdata/genes 4: /cgn2_2/gcgdata/genes	5: /cgn2_2/gcgdata/geneseq. 6: /cgn2_2/gcgdata/geneseq.	/cgn2_2/	/ Cgn2/	the numb than or than or	SUMMARIES		Match Length DB ID	.6 22 19 .6 22 19	6 972 20	.6 1661 20 6 4197 16	59.1 396 20 X34752 59.1 828 20 216735 59.1 1079 20 X20676	.1 1482 19 .1 1786 18
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            This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainel. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
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Magnosis; ss.
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llarity 63.6%; Pred. No. 33;
Conservative 0; Mismatches
                                                                                                                                     diagnosis of past or present LS infection.
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Best Local Si
Matches 14;
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This sequence represents a Leptospira DNA sequence isolated from the pathogonic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
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Mismatches
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1 tgttggatcacaagatttgata 22
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ID X99627 standard; DNA; 972 BP.
                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97AU-0005494
                                                                                                                                                                                                                                                                                                                                                  20-JAN-1999 (first entry)
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                                                                                                                                                                                                                     V58900 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-520791/44.
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leptospira sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9840099-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chappel RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                        V58900
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Score 14; DB 19; Pred. No. 33; 0; Mismatches 8

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63.6%; ilarity 63.6%; Conservative

Query Match Best Local Similarity Matches 14; Conserv

Length 22;

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us-09-380-826a-6.rng

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pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for prophylactic or detection and diagnosis of past or present LS infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a Leptospira DNA sequence isolated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Hsp60-2; immune response; immunological carrier; rrol; tumour; sarcoma; cancer; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.
                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Length 1477;
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Pred. No. 56;
0; Mismatches
                                                                                                                                                                                        (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
(PIGR-) PIG RES & DEV CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         developing products for conferring pro
prophylactic or therapeutic treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 69-70; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 tgttggatcacaagatttgata 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 63.6%;
Local Similarity 63.6%;
les 14; Conservative
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                                                                        98WO-AU00145
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                                                                                                                                97AU-0005494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes
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                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-520791/44
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                                                                        06-MAR-1998;
                                                                                                                                07-MAR-1997;
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         17-SEP-1998
                                                                                                                                                                                                                                                                                           Chappel RJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mizzen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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         δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Ureaplasma urealyticum infection. It provides novel genes (x99501-681) that can be used as a source of primers and probes for the detection and or quantification of U. urealyticum in a biological sample. The probes that can be used in the method of the invention by forming target: probe complex is copmolementary to a region selected from one of the 181 nucleic acid sequences (x99501-681). U. urealyticum is an opportunistic pathogen of the human urogenital tract that is a significant cause of the human urogenital tract that is a significant cause of the infections are commonly asymptomatic, it is important to have specific and sensitive methods for detecting their presence in a patient. Also, as the pathogen has no current antibiotic directed specifically against it, it would be advantageous to isolate and detect gene sequences which are unique to it, and utilise these as a basis for diagnosis of urealyticum infection as well as to develop new and improved drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention provides methods for the detection and diagnosis
Ureaplasma urealyticum; nucleic acid detection; infection; pathogen; human urogenital tract; pregnancy; neonatal disease; drug therapy; suppurative arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapies. The present invention provides such novel polynucleotide sequences (X99501-681).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of Ureaplasma urealyticum using novel genes, probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glass JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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63.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glass JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 82; 110pp; English.
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                                                                                                                                   Ureaplasma urealyticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UABR-) UAB RES FOUND
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es 14; Conserv
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Disclosure; Fig.6; 95pp; English.
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                                                                                                      The present sequence encodes a heat shock protein, designated Hsp60-2. The protein, its fragments, variants and fusion proteins, are used to elloit or enhance an immune response against Streptococcus, and to elloit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated of used antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, overy, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Surface layer protein; SLP; fusion protein; vaccine; antigen; surface expression; epitope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutically in gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                Claim 3; Fig 4A-B; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dhaese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%;
63.6%;
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/*tag= b
95..184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
185..3850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79..85
/*tag=
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P-PSDB; R80530.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9519371-A2
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Q99430/c
\mathbf{x} \otimes 
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Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in Y06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in Y06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
A probe based on the N-terminal sequence of B. sphaericus P-1 (LMG 9-13855) surface layer protein was used to screen an Hindili-generated library to isolate the slp gene. Promoter regions of the gene are used in genetic constructs providing surface expression of heterologous proteins in P-1 hosts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
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                                                                                                                                                                                                                                                           DB 16; Length 4197;
63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.1%; Score 13; DB 20; Length 396; 61.9%; Pred. No. 1.7e+02; ive 0; Mismatches 8; Indels
                                                                                                                                                                   Sequence 4197 BP; 1470 A; 731 C; 763 G; 1233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 396 BP; 147 A; 49 C; 58 G; 142 T; 0 other;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                        Score 14;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 12A; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      2836 TGTTGGAGCAACTGGTTTGATA 2815
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                                                                                                                                                                                                                                                                                                                                                                    1 tgttggannnnnnntttgata 22
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                                                                                                                                                                                                                                                     63.6%;
63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding OMP-1T protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X34752 standard; DNA; 396
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6 Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia chafeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-254290/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer. The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                            Human gene expression product cDNA sequence SEQ ID NO:4205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human genes and their expression products which are differentially expressed in different cell types
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1992; 2479pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide analogues and antagonists.
                                                                                            216735 standard; cDNA; 828 BP.
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98US-0075954
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Lamson G, Leshkowitz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-494092/41.
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                                                                                                                                                                                                                                                                                          12-0CT-1999
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24-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1998;
03-APR-1998;
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                                                                                                                                                                                              216735;
6
RESULT
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Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal aplasia; vesical-ureteral reflux; pelvi-ureteral junction obstruction; multicystic renal dysplasia; renal agenesis; hydronephrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detectidiseases related to Borrella infections in animals, and for the
                                                                                                                                                                                                                               Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X20500-21243 represent polynucleotide sequences from the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                               Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.1%; Score 13; DB 20; Length 1079; 61.9%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of breakpoint region on chromosome 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1079 BP; 397 A; 280 C; 181 G; 221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production of biosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 842-843; 1150pp; English.
                199 tgttggagaattcattttgnta 220
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22
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                                                                                                                                                                                                                                                                                                                                                                      98WO-US13041.
                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
1 tgttggannnnnnntttgata
                                                                                                                                                                                                                                                                                                                                                                                                   97US-0050667
                                                                                                      X20676 standard; DNA; 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 gttggannnnnntttgata
                                                                                                                                                                05-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                               enzyme production;
                                                                                                                                                                                                                                                                           Treponema pallidum
                                                                                                                                                                                                                                                                                                        WO9859034-A2.
                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                        30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser CM;
                                                                                                                                   X20676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V18099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
V18099
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Gaps

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Length 828;

Score 13; DB 20; Length 82 Pred. No. 1.8e+02; 0; Mismatches 9; Indels

0;

59.1%;

Query Match 59.1 Best Local Similarity 59.1 Matches 13; Conservative

Mitogen activated protein kinase; MAP; infectious specific protein; plant; jasmone acid; ss.

MAP kinase #2 coding sequence.

04-JUN-1997

T60350;

RESULT 12 T60350/c

T60350 standard; cDNA to mRNA; 1786 BP

268 tgttggattttcctctttgat 288

q

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reflux, uni or bilateral pelvi-ureteral junction obstruction, multicystic renal dysplasia, renal agenesis, renal aplasia, hydronephrosis, von Mayer-Rokitansky-Kuester disorder and bifid ureter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This represents the nucleotide sequence of the breakpoint region on der(19) which reveals that the transcriptional orientation of the hydronephrosis (HKG) gene on the short arm of chromosome 6 is from the telomere to the centromere. A translocation partner to this gene on chromosome 6 is the chromosome 19 USF2 gene. The HNG gene can be used as a starting point to design suitable compounds or techniques for the treatment of renal diseases or disorders, or nucleotide probes for diagnosing cells involved in renal diseases or disorders. A protein or preparing suitable antibodies for diagnosing cells involved in renal diseases and disorders. The products and method can be used to treat or diagnoses ernal diseases and disorders and method can be used to treat or diagnose renal diseases and disorders evaluation or the contraction of the contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydronephrosis gene - useful to treat or diagnose renal diseases and disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction obstruction, multicystic renal dysplasia or renal agenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note "partial sequence of exon 7 of USF2 gene; the transcriptional orientation is from the
                                                                                                                                                          /*tag= a
/note= "sequences derived from chromosome 6p21."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
/note= "chromosome 19-derived USF2 sequences"
1466..1477
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                                                                                                                                                                                                                                                          /note= "partial intronic sequence of HNG"
Von Mayer-Rokitansky-Kuester disorder; bifid ureter; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         centromere to the telomere"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
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                                                                                                                                                                                                                                                                                                                          /number= 9
/note= "exon 9 of HNG"
                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= d
/note= "Alu repeats"
1223..1482
                                                                                                  Location/Qualifiers
1..1222
/*tag= a
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/number= 7
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/*tag= b
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356..533
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                                                       Homo sapiens
                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                                                                                       Kev
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Wound-stress inducible MAP kinase - used to regulate the synthesis

(NORQ) NORINSUISANSHO NOGYO SEIBUTSU SHIGEN

WPI; 1997-220416/20. P-PSDB; W15513.

of jasmone acid

95JP-0220935

29-AUG-1995;

JP09065881-A.

Synthetic.

11-MAR-1997,

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                                                                                                                                                                                                                                                                                                                                                            T60349 and T60350 represent the coding sequences for the mitogen activated protein (MAP) kinases of the invention. The protein encoded by this sequence contains the T-E-Y sequence, in which the threonine and tyrosine residues are phosphorylated to activate the protein at residues 249-231. The MAP kinase and its gene can be used to regulate the synthesis of jasmone acid and the synthesis of a group of infectious synthesis of jasmone acid and the MAP kinase gene into a plant, thereby inducing expression of the MRNA kinase (or its antisense proteins can be regulated in the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virulence; P7C18; vaccine; antibacterial; antibiotic; screening; phosphoribosylformylglycinamide decarboxylase; PurL; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1786 BP; 503 A; 390 C; 353 G; 540 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus mutant P15C31 virulence gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 14-16; 21pp; Japanese.
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Matches 13; Conservative
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Gaps

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1 tgttggannnnnnntttgat 21

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Best Local Similarity Matches 13; Conserva

Query Match

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somitogenesis zebrafish cDNA libraries with a probe corresponding to the Drosophila melanogaster FTZ-Flalpha DNA binding domain. The isolated clones can be used to produce RXR delta and espsilon polypeptides useful for modifying retinoid activity and identifying specific target genes implicated in retinoid responses important in
                                                                                                                                                                                                                                           Isolated retinoid X receptor protein - having amino acid insert in ligand binding domain, useful to identify specific target genes implicated in retinoid responses important in disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRBAP-1; carbohydrate-associated protein 1; human; autoimmune disorder; inflammathon; gastrointestinal disorder; infection; reproductive disorder; neurological disorder; eye disorder; cell proliferation; cancer; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "a polynucleotide containing C at position 428 is specifically claimed in Claimed 21"
                                                                                                                                                                                                                                                                                                                                                          cDNA clones (T67196 and T67197) respectively code for novel retinoid X receptors RXR delta (W18032) and RXR epsilon (W18033) that exhibit a high degree of amino acid conservation with other vertebrate RXRs but which represent unique subtypes defined by an additional 14-amino acid segment in their ligand binding domains. The RXR epsilon clone was isolated by screening adult and post-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13; DB 18; Lengtn 25. Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2508 BP; 600 A; 652 C; 646 G; 610 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human carbohydrate-associated protein CRBAP-1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          Claim 8; Page 29-30; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /frequency= "0.10"
                                                                                                                                          Petkovich M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2424 tgttggacatgagtttttgat 2444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                  (TOOH ) UNIV QUEENS KINGSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.1%;
61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294941/c
ID 294941 standard; cDNA; 3519
                   96CA-2177642.
                                                         95US-0462182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.1
Best Local Similarity 61.9
Matches 13; Conservative
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                                                                                                                                                                                 WPI; 1997-298660/28
                                                                                                                                          Ohno C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200018922-A2.
                                                                                                                                                                                                      P-PSDB; W18033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease states
                   29-MAY-1996;
                                                         05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000
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                                                                                                                                          В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294941;
                                                                                                                                          Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of a virulence gene identified in Staphylococcus aureus mutant P15C11. S. aureus genes (see X07088-136) associated with virulence were identified by signature-tagged mutagenesis in which mutants containing a chromosomal insertion of a signature tagged transposon were generated, mutants with attenuated virulence were identified in amouse model of bacteraemia, and the nucleotide sequences of the regions flanking the transposon insertion sites of these mutants were determined. Database sequence comparisons were performed to identify the virulence genes and to determine the possible function of their protein products (see also W97680-724). The P15C31 virulence gene product (see W97694) was identified as phosphoribosylformylgycinamide decarboxylasse Purt., an enzyme involved in purine biosynthesis. A claimed method of identifying an antibacterial agent involves assaying potential agents for the ablility to interfere with the expression of S. aureus containing a neutional mutation in one of the virulence genes, and its use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps

    useful

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                                                                                                                                                                                                                                                                                                                        Inhibition of virulence genes from Staphylococcus aureus for, e.g. screening for potential anti-microbial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2190 BP; 753 A; 309 C; 461 G; 666 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 20; L
Pred. No. 2.1e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retinoid X receptor; RXR epsilon; zebrafish; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zebrafish retinoid X receptor RXR epsilon cDNA.
                                                                                                                                                                             (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 86-89; 203pp; English.
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388..1704
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Best Local Similarity 61.9%;
Matches 13; Conservative
                                                                                                  98WO-GB01974.
                                                                                                                                      97US-0887534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine compositions
                                                                                                                                                                                                                                                              WPI; 1999-105999/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio.
                                                                                                                                                                                                                                                                               P-PSDB; W97694
                 W09901473-A2
                                                                                              03-JUL-1998;
                                                                                                                                      03-JUL-1997;
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                                                       14-JAN-1999
                                                                                                                                                                                                                       Holden DW;
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Gaps

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Length 2508;

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PR 29-SEP-1999; 99WO-US22685.

XX 01-OCT-1998; 98US-0167195.
PR 06-OCT-1998; 98US-0167195.
PR 06-OCT-1998; 98US-0167195.
PR 01-DEC-1998; 98US-0167195.
PR 01-DEC-1998; 98US-0167196.
XX M. MPI; 2000-317516/27.
PR 04VOUR JJ. Lal P. Bandman O. Reddy R. Baughn MR. Yue H; Hilman JJ. Robert Carbon Carb
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Ouery Match 59.1%; Score 13; DB 21; Length 3519; Best Local Similarity 61.9%; Pred. No. 2.2e+02; Matches 13; Conservative 0; Mismatches 8; Indels 0; Gaps
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1909 TGTTGGAGTCACCTGTTTGAT 1889

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Search completed: March 27, 2001, 08:23:01 Job time: 5303 sec

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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sim
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
0000
                                                                          (without alignments)
26.799 Million cell updates/sec
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Sequence 8, Appli
Sequence 19, Appli
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Appli
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                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1,
Sequence 3,
Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5
Sequence 1
Sequence 1
Sequence 1
Sequence 5
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-714-918-19
US-08-714-918-19
US-08-473-446-118
US-08-752-238-2
US-09-085-6038-2
US-09-085-6038-2
US-09-08-39-129-1
US-08-339-129-1
US-08-752-238-1
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US-09-136-652-1
US-08-670-707A-38
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US-08-212-133A-5
US-08-474-503-3
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PCT-US93-03275-1
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US-09-031-897-5
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US-07-864-004B-1
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                                                                                                                          tgttggannnnnnntttgata 22
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                                              - nucleic search, using sw model
                                                                March 27, 2001, 08:19:22
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Maximum DB seq length: 2000000000
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22
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Match Length
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; Patent No. 5874267
; GENERAL INFORMATION:
: TITLE OF INVENTION: Expression of surface layer proteins
: TITLE OF INVENTION: Expression of surface layer proteins
: TITLE OF INVENTION: Expression of surface layer proteins
: TITLE OF INVENTION: 25
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: COMPUTER: IBM PC compatible
: COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/682,517
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TITLE OF INVENTION: Expression of surface layer proteins
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
US-09-058-489-20
US-08-35-555-1
US-08-670-708-36
US-09-088-489-21
US-09-280-739-1
US-08-280-739-1
US-08-280-739-1
US-08-86-111D-15
US-08-46-23
US-09-044-908-23
US-09-044-908-23
US-09-044-908-23
US-09-184-658-11
US-08-419-009-19
US-08-419-009-10
US-08-419-009-10
US-08-419-009-10
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Mismatches
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63.6%; Pred. No.
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; Sequence 14, Application US/08682517
; Patent No. 5874267
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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14; Conservative
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66057
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6727
13011
40352
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Score 14; DB 2; Length 4197;
Pred. No. 25;
0; Mismatches 8; Indels
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COmpatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: MOLGATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FITTING DATE: September 13, 1996
         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
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10S-08-714-918-19
Sequence 19, Application US/08714918
Patent No. 6037123
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APPLICATION NUMBER: 60/009,102
                                                                                                                                                                                                                     ORGANISM: Bacillus sphaericus
INDIVIDUAL ISOLATE: P-1
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STREET: 633 West Fifth Street
STREET: Suite 4700
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                                                              CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 4197 base pairs
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Best Local Similarity 63.6
Matches 14; Conservative
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185..3850
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95..184
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APPLICANT: Benton, Bret
                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                          95..3850
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                              TOPOLOGY: linea
MOLECULE TYPE: DN
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                            NAME/KEY:
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US-08-682-517-8
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Pred. No. 25;
0; Mismatches 8; Indels
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25;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression of surface layer proteins
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APPLICATION NUMBER: US/08/682,517
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Pred. No. 25;
0; Mismatches
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08682517 Patent No. 5874267 GENERAL INFORMATION: APPLICANT:
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2836 TGTTGGAGCAACTGGTTTGATA 2815
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Patent No. 5874267
GENERAL INFORMATION:
APPLICANT:
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FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3666 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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; MOLECULE TYPE: DNA (genomic)
US-08-682-517-7
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Best Local Similarity 63.6%;
Matches 14; Conservative
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63.6%;
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 4197 base pairs
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NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy discompa
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EDNESS: single
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; LOCATION: 1..3
US-08-682-517-14
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STRANDEDNESS:
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US-08-682-517-8/c
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APPLICANT: PAGLETI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
TITLE OF INVENTION: LADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
             Gaps
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Pred. No. 1.7e+02;
0; Mismatches 9; Indels
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APPLICANT: Mohr Dr., Georg
APPLICANT: Saldanha Dr., Roland
APPLICANT: Matsuura Dr., Manabu
TITLE OF INVENTION: Method for Preparing Nucleotide
TITLE OF INVENTION: Integrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,446
           6
         0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/POCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEW YORK
: UNITED STATES OF AMERICA
                                                                                                                                                            RESULT 7
US-08-473-446-118
; Sequence 118, Application US/08473446
; Patent No. 6017542
; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08752238 Patent No. 5804418 GENERAL INFORMATION:
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                                                                                              1076 TGTTGGATAACTATTTTTATA 1097
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TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
                                                     1 tgttggannnnnnntttgata 22
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59.1%;
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Best Local Similarity 59.1
Matches 13; Conservative
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NE COUNTRY:
         13;
         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PAOLETII, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1760;
                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 5253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPSY disk
COMPUTER: PATENTINE FO-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.4; DB 1;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                              59.1%; Score 13; DB 61.9%; Pred. No. 94; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 25,506
TELECOMMUNICATION INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEEAX: 67-310
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/413,118 FILING DATE: 29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 118, Application US/08413118 Patent No. 5688920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 2895 GTTGGATGTGTTTTGATA 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 118:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 gttggannnnnnntttgata 22
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59.1%;
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LENGTH: 1760 base pairs
                                                                                                                                                                                                                                                                                                                                                            Query Match 59.1
Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: CDN. US-08-413-118-118
                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-714-918-19
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Best Local Similarity
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APPLICANT: Lambowitz, Alan
APPLICANT: Lambowitz, Georg
APPLICANT: Mont, Georg
APPLICANT: Junerly, Steven
APPLICANT: Junerly, Steven
APPLICANT: Guo, Huatao
TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.4; DB 3;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.7e); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 800 Superior Avenue, Suite 1400 CITY: Cleveland
                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24671/04000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calfee, Halter & Griswold
                                                US/09/085,603B
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APPLICATION NUMBER: US/09/031,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-031-897-6/c
; Sequence 6, Application US/09031897
; Patent No. 6027895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ||||||
| 139 TATTGGAATATAAATTTTGATA 118
                                                                                                                                                                                                   TELEPHONE: (216) 622-8416
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH 1800 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tgttggannnnnnntttgata 22
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: DOCHETLY, Pamela A.
REGISTRATION NUMBER: 40.591
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
TELEPHONE: (216)542-8416
TELEFAX: (216)241 0816
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.48;
59.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.4
Best Local Similarity 59.1
Matches 13; Conservative
                         CURRENT APPLICATION DA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 1..1800
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                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-09-085-603B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yang Dr., Jiam
APPLICANT: Yang Dr., Jiam
APPLICANT: Zimmerly Dr., Steven
APPLICANT: Guo Dr., Huather
APPLICANT: Gall Dr., Clifford J.
TITLE OF INVENTION: Methods of Making an Rnp Particle
TITLE OF INVENTION: Having Nucleotide Integrase Activity
NUMBER OF SCOURENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                 ZIP: 44114

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.4; DB 1;
Pred. No. 1.7e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALFEE, HALTER & GRISWOLD LLP
                           ADDRESSEE: CALFEE, HALTER & GRISWOLD STREET: 800 Superior Avenue CITY: Cleveland STATE: Ohio COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                            24671/00103
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/752,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09085603B
Patent No. 6001608
GENERAL INFORMATION:
APPLICANT: Lambowitz Dr., Alan M
APPLICANT: Saldanha Dr., Roland
APPLICANT: Saldanha Dr., Roland
APPLICANT: Matsuura Dr., Manabu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: GOLIACK, MARY E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 24671
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 221-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 TATTGGAATATAAATTTTGATA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.4%;
Best Local Similarity 59.1%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1800 base pairs
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-752-238-2
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APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH:
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STATE:
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                                                                                                                                                                                 Query Match 56.4%; Score 12.4; DB 3; Length 1800; Best Local Similarity 59.1%; Pred. No. 1.7e+02; Matches 13; Conservative 0; Mismatches 9; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USS

ZIP: 75270-2197

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN RC-BOS/MS-DOS
SOFWARE: PATENTIN RC-BOS/MS-DOS
SOFWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,129
FILING ATTENTION NUMBER: US/08/339,129
RIGISTATION NUMBER: 31,966
ATTORNEY/AGENT NUMBER: 31,966
REFERENCE/DOCKET NUMBER: NOBF B35969
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFRAX: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08339129
Patent No. 5750399
GENERAL INFORMATION:
APPLICANT: Dixon, Richard A.
APPLICANT: Palva, Nancy L.
APPLICANT: Commen, Abraham
TITLE OF INVENTION: Isoflavone Reductase Promoter
TUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Db 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Richards, Medlock & Andrews
1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-752-238-1/c
; Sequence 1, Application US/08752238
                                                                                                                                                                                                                                                                                            139 TATTGGAATATAAATTTTGATA 118
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                                                                                                                                                                                                                                                                   1 tgttggannnnnnntttgata 22
                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2730 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
double
                                                                                                1..1800
                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lineaı
                                                                             ; NAME/KEY: CDS
; LOCATION: 1..1
US-09-031-897-6
STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE:
US-08-339-129-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Dallas
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 120
                                                                                                                                                                                                                                                                                                                                                                                         US-08-339-129-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zimmerly Dr., Steven
APPLICANT: Guo Dr., Huatao
APPLICANT: Beall Dr., Clifford J.
TITLE OF INVENTION: Methods of Making an Rnp Particle
TITLE OF INVENTION: Having Nucleotide Integrase Activity
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALFEE, HALTER & GRISWOLD LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
APPLICANT: Mohr Dr., Georg
APPLICANT: Saldanha Dr., Roland
APPLICANT: Saldanha Dr., Roland
APPLICANT: Massuura Dr., Manabu
TITLE OF INVENTION: Method for Preparing Nucleotide
TITLE OF INVENTION: Integrase
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALFFF ....
STRFFF
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE STREET: CALFEE, HALTER & GRISWOLD LLP STREET: 800 Superior Avenue STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                     ADDRESSEE: CALFEE, HALTER & GRISWOLD STREET: 800 Superior Avenue CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 24671/00103 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lambowitz Dr., Alan M
Mohr Dr., Georg
Saldanha Dr., Roland
Matsuura Dr., Manabu
Yang Dr., Jiam
Zimmerly Dr., Steven
Guo Dr., Huatao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-085-603B-1/c
; Sequence 1, Application US/09085603B
; Patent No. 6001608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLFICK, MATY E.
REGISTRATION NUMBER: 34,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tgttggannnnnnntttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 13; Conserva
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US-08-752-238-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                     COUNTRY: US
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APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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4; ... 1.8e+02; ... 9; Indels

0; Mismatches

Length 2761;

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56.4%; Score 12.4; DB 3; 59.1%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                          1 tgttggannnnnnntttgata 22
                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
LENGTH: 2761 base pairs
                                                                                                                                                           Query Match
Best Local Similarity 59.19
Matches 13; Conservative
                                           double
                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
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                      TYPE: nucleic
STRANDEDNESS:
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APPLICANT: Lambowitz, Alan
APPLICANT: Lambowitz, Alan
APPLICANT: Jamen's Georg
APPLICANT: Gloo, Huatao
TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide
TITLE OF INVENTION: Integrases
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold
STREET: 800 Superior Avenue, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,603B
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/031,897
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Pred. No. 1.8e+02;
                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DOCHETY, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/ODCKET NUMBER: 24671/04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8416
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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NAME: Docherty, Pamela A.
RECISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24671/00105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216)622-8416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09031897
Patent No. 6027895
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MOLECULE TYPE: DNA (genomic)

US-09-085-603B-1
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Best Local Similarity 59.1%;
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                   FILING DATE:
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STATE: Ohio
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APPLICANT: Barkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Loosmore, Sheena M.
APPLICANT: Van.Pan
APPLICANT: Yan.Pan
APPLICANT: Yan.Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/613,009A FILING DATE: .08-WAR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.4; DB 3;
Pred. No. 1.9e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                     US-08-613-009A-1/c
; Sequence 1, Application US/08613009A
; Patent No. 6090576
890 TATTGGAATATAAATTTTGATA 869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tgttggannnnnnntttgata 22
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59.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       APPLICANT: Myers, Lisa E APPLICANT: Schryvers, Ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3438 base pairs
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Best Local Similarity 59.1
Matches 13; Conservative
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STRANDEDNESS: single
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Search completed: March 27, 2001, 08:19:23 Job time: 5150 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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25:* 26:* 27:* 28:*	of results predicted qual to the score of t sis of the total score	SUMMARIES	. DB ID	28 BB35778	34 BE05964	38 BE9560	6 AI122094	6 AW879900	26 BB2879	AA515145 05 RE20275	56 AZ0372	AV54687	7 AW225U52	19 AQ10	53 AQ84447	AM24046	14 R892	3 AW624588	49 AQISU6 AA555292	59 AQ5497	3 AI662442	36 BE8543	28 AL370583	2 A159192 54 A09146	46 T75954	/4 B29252	03 BE4482) AA637362	59 AQ5898	7/ BE35341	3 AW649760	0 AW41357	3 AW648609	60 AQ6692	7 AT99730	0 AW39835	AV6786
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BB357781 184 bp mRNA EST 12-JUL-2000 BB357781 RIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030024G02 3', mRNA sequence. BB357781.1 GI:9069609 BEST. house mouse.
BB357781 184 bp mRNA BB357781 RIKEN full-length enz musculus CDNA clone C030024G02 BB357781 GI:9069609 EST. house mouse.
BB357781 BB357781 RIK MUSCULUS CDN BB357781 BB357781.1 BEST. house mouse.
RESULT 1 BB357781/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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KEYWORDS
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URL:http://genome-resertcriken.go.jp,
URL:http://genome-resertcriken.go.jp/
URL:http://genome-rtc.riken.go.jp/
URL:http://genome.rtc.riken.go.jp/
Carninci.P., Nishiyama.Y., Westover.A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Y. and Hayashizaki,Y. Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and mayashizaki,Y. (1999)
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                       E 1 (bases 1 to 184)

S Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Kiyosawa, H., Kojima, Y., Mizin, M. Sakai, C., Sato, K., Shibata, Y., Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Y., Suuki, H., Suzuki, H., Yaqawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yokota, T., Yoshida, K., Yoshiho,
RIKEN Mouse ESTS (Konno, H., et al.)
Contact: Yoshihide Hayashizaki
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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 184)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                         REFERENCE
AUTHORS
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FEATURES

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/note="Vector: paluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XLIO-Gold host cells. This library was
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L (bases 1 to 210)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Mattin,J., Beck,C., Wile,T., Underwood,K., Stephoe,M., Theisling,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,P., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                  BE059640 210 bp mRNA EST 09-JUN-2000 sn35a01.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-13441 5' similar to TR:Q9ZVI3 Q9ZVI3 PUTATIVE ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales, Fabaceae, Papilionoldeae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkway Circle St. Louis, Missouri 63134 For further information acall: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@enomesystems.com or info@enomesystems.com web site: www.genomesystems.com Seq primer: 408F from Gibco High quality sequence stop: 165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="immature flowers of field grown plants"
/lab_host="XL10-Gold"
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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0
          Length 184;
                                                                                   Indels
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             Score 14; DB 128;
Pred. No. 6.5e+02;
                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR, ;, mRNA sequence.
                                                                                                                                             1 tgttggannnnnnntttgata 22
                                                                                                                                                                                    82 TGTTGGAAATGGCTTTTGATA 61
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          63.68;
63.68;
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Query Match
Best Local Similarity 63.69
Matches 14; Conservative
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us-09-380-826a-6.rst

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ORIGIN

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/db_xxef="laxon:10000"
/db_xxef="laxon:10000"
/clone="UI-W-BH4-bav-a-11-0-UI"
/clone="UI-W-BH4-bav-a-11-0-UI"
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site=1: Not I; Site=2: Eco Ri; The NIH_BMAP_M_S5 library is a subtracted library of a series ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygadala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of coNNA from which ESTS had already been generated. For a detailed description of the library from which this clone was derived, please visit our web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
7el: 301 443 1706
Fax: 301 443 9890
Email: merremail.nih.gov
The sequence contained an oligo-dr track that was present in the oligoucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site strand cDNA and therefore this may represent he NotI site olfactory bulbs tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from ReSERKH GENETICS. It should be noted that Bento Soares Lab generating a small number of additional specialized non-redundant appropriate and limited collaborative arrangements
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                     BE956026 228 bp mRNA EST 04-OCT-2000 UI-M-BH4-bav-a-11-0-UI.SI NIH_BMAP_M_SS MUS MUSCUlus CDNA clone UI-M-BH4-bav-a-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 228)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                          Gaps
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           DB 134; Length 210;
                                                                    8; Indels
        Score 14; DB 134;
Pred. No. 6.7e+02;
0; Mismatches
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TAG_LIB=NIH_BMAP_M_S5
TAG_TISSUE=olfactory-bulbs
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BE956026.1 GI:10600157
  ch 63.6%;
1 Similarity 63.6%;
14; Conservative
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Matches 14; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;
Bukaryota; Metazoa; Chordata; Sciurognath!; Muridae; Murinae; Mus.
Romo, H., Alazwa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.
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Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Soqabe, Y., Sugahara, Y.
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Y., Taunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
W., Muramatau, M. and Hayashizaki, Y.
KIKEN Mouse ESTS (Konno, H., et al.)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
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Email: genome-resertc riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci.P. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Y. and Hayashizaki,Y. Ozawa,Y., Muramatsu,M., Okazaki Automated filtration-based high-throughput plasmid preparation Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 BB170254 EST 29-JUN-2000 BB170254 RIKEN full-length enriched, adult male hypothalamus Musculus cDNA clone A230017D13 3', mRNA sequence.
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/clone_lib="RIKEN full-length enriched, adult male
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                                                                                                                                               Length 228;
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                         Score 14; DB 138;
Pred. No. 6.8e+02;
                                                                                                                                                                                          0; Mismatches
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TAG_SEQ=CAAGG"
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                             47 c
                                                                                                                             Query Match
Best Local Similarity 63.61
Matches 14; Conservative
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                       64 a
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LOCUS
DEFINITION
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ORIGIN
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JOURNAL
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KEYWORDS
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Anote—"Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary polylinker; 1st strand cDNA was prepared from mammary polylinker; 1st strand cDNA was listate from a lactating femele, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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Frax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-Qv3-OT0029-290
300-134-b02&t3-2000-03-29&t4-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 261)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., deOliva,M.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW879900 261 bp mRNA EST 23-MAY-2000
QV3-OT0029-290300-134-b02 OT0029 Homo sapiens CDNA, mRNA sequence.
AW879900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shorgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                       Score 14; DB 16; Length 250;
Pred. No. 6.9e+02;
0; Mismatches 8; Indels
                    /tissue_type='mammary gland"
/lab_host="DH10B"
/sex="female (lactating)"
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/db_xref="taxon:9606"
/clone_lib="070029"
/dev_stage="Adult"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 250)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                /note—"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [8]
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IMAGE:1401067 5' similar to SW:Y335_MYCGE P47577 HYPOTHETICAL
GTP-BINDING PROTEIN MG335.;, mRNA sequence.
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Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.6%; Score 14; DB 102; Length 235; 63.6%; Pred. No. 6.9e+02; ive 0; Mismatches 8; Indels
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/db_xref="taxon:10090"
/clone="IMAGE:1401067"
/clone_lib="Soares_mammary_gland_NMLMG"
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High quality sequence stop: 225.
Location/Qualifiers
1. .250
                  /tissue_type="hypothalamus"
/dev_stage="adult"
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The WashU-HHMI Mouse EST Project
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                                                              host="DH10B"
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Matches 14; Conservative
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ENKAROPCAS, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 265)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, F., Kukuda, Y., Hara, A., Hayatau, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Kajosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shipata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Sunoda, Y., Wataniki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yasunishi, H., Yakawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yasunishi, H., Yakawa, A., Takahashi, F., Tominaga, N., Toya, M., Muramatsu, M. and Hayashizaki, Y. Yoshida, K., Yoshiki, A., Yoshino, H., Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-resertc.riken.go.jp,
Carninoi,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninoi,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoatchization of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
                                                                                                                                                                  Gaps
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/tissue_type="egg"
/dev_stage="2 cells"
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                                                                                                          DB 96; Length 261; 7e+02;
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                     Score 14; DB 9
Pred. No. 7e+02
0; Mismatches
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COMMENT

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/note="Site_1: Sall; Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken primed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGACACAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
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information can be
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( Dases 1 to 298)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute; Cancer Genome Anatomy Project (CGAP),
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Pred. No. 7e+02;
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/tissue_type="liposarcoma"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 tgttggannnnnnntttgata 22
                                                                                                                                                                                                                                                                                                                                                                63.6%;
63.6%;
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56:5380-5383.
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Unpublished (1997)
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us-09-380-826a-6.rst

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157 TGTTGGATTGATGGGTTTGATA 178
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63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends.
                                                                                                                                                                                                                               Mus musculus
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AZ037213
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AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnollophyta; eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales, Fabaceae, Papilionoideae, Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 332)
AndenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="genotype A17"
/db_xref="teaxon:3880"
/clone="pkV1-3023"
/clone_lib="kV1"
/tissue_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTs from roots of Medicago truncatula 24 hours after inoculation with Sinorhizobium meliloti
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                                                                                                                                                                                                                                                                                      07-SEP-2000
                                                                                                                                                                                                                                                                                    BE202756 332 bp mRNA EST 07-SEP-2000
EST402778 KV1 Medicago truncatula cDNA clone pKV1-3023, mRNA
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                                                                          Length 298
                                                                        Score 14; DB 8; Length 296
Pred. No. 7.2e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Katemail.bio.tamu.edu
Texas A&M University:T262522e
TIGR sequence name:MTARE96TK
More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: VandehBosch K
Department of Biology
Texas A&M University
College Statilon, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
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91
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BE202756.1 GI:8746021
                                                                          63.68;
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                                                                                            Local Similarity
les 14; Conserv
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BASE COUNT
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BHOR electrocompetent cells (BRL Life Technologies). "
37 c 45 g 157 t
A2037213 336 bp DNA GSS 01-MAR-2000
RPCI-23-364L15.TV RPCI-23 Mus musculus genomic clone RPCI-23-364L15
CONA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                     Zhao.S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Szhaofeigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter/dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: 77
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 336)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, 18712 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 7.4e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="RPCI-23-364L15"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_GSSs: RPCI-23-364L15.TJ
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J
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SOURCE

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/lab_host="E. coli BM25.8"

/note="Organ: shoot tips: Vector: Lambda TriplEx; Site_1:
Sfi1 (A); Site_2: Sfi1 (B); Shoot tips (approx. 2 cm from
apex) were collected during the spring, frozen and used
for mRNA isolation. The SMARY-PCR method (Clontech) was
used to prepare a library from 1 ug total RNA, using the
Lambda TriplEx vector. Plasmid subclones in pTriplEx were
recovered by cre-lox excision in E. coli strain BM25.8 and
a 48 c 74 g 136 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 371)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC_ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hbeetigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
a 69 c 85 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ311167 371 bp DNA GSS 22-DEC-1998
CITBI-E1-2525E11.TR CITBI-E1 Homo sapiens genomic clone 2525E11,
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                                                                                                                                                                                                                                                                                                    Length 364;
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                                                                                                                                                                                                                                                                                           Score 14; DB 87; Length 36
Pred. No. 7.5e+02;
0; Mismatches 8; Indels
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Best Local Similarity 63.68; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="2525E11"
/clone_lib="CITBI-E1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence.
A0311167
A0311167.1 GI:4042980
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63.6%;
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Best Local Similarity 63.6'
Matches 14; Conservative
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                                                           Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Guicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 359)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of coNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and 10NA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                           Contact: Erika Asamizu
He First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Emall: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
1. 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
,NC, 27695-8008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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AW226052 1 GI:6555348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Arabidopsis thaliana roots Columbia"
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Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R. The Pine Gene Discovery Project
Unpublished (1999)
Contact: Ross Whetten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 359;
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/db_xref="taxon:3352"
/clone="S776G08"
/clone_lib="Pine TriplEx shoot tip library"
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Seq primer: 5' lambda TriplEx2 Sequencing Primer.
Location/Qualifiers
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/organism="Arabidopsis thaliana"
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Pred. No. 7.5e+02;
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/db_xref="taxon:3702"
/clone="RZL21a12F"
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Fax: 919-515-7801
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                                              thale cress.
      AV546877.1
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Contact: Martienssen RA
Cond Spring Harbor Laboratory
1 Bungtown Rd., Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8322
Fax: 516 367 8369
Email: martiens@cshl.org
Seq primer: forward
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 27, 2001, 07:38:25
Job time: 4588 sec
                                                                                                                                                                                                          /organism="Zea mays"
                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity 63.6%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Liliopsida; Poales; Poaceae; Zea.

1 (bases 1 to 376)
Rabinowicz, P.D., Schutz, K., Dedhia, N., Yordan, C., Parnell, L.D.,
Stein, L., WacComble, W.R. and Martienssen, R.A.
Differential methylation of genes and retrotransposons allows
shotgun sequencing of the maize genome
Nat. Genet. 23, 305-308 (1999)
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                                                                                                         AQ102282 376 bp DNA GSS 27-AUG-1998 HS_3029_A2_G04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=8 Row=M, DNA sequence.
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1. 376.../
1. 376.../
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3029 Col=8 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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an3791J JM101 filtered library Zea mays genomic, DNA sequence.
AQ844476.1 GI:6202964
                                                                                                                                                                                                                                                                                                                                                                                    scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jWallace@u.washington.edu
Sequence Tagged Connector
Plate: 3029 row: M column: 8
Class: BAC ends
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276 TGTTGGAATTACAGGTTTGATA 255
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Length 376; Indels

Score 14; DB 163; Pred. No. 7.5e+02; 0; Mismatches 8;

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Maize acetyl CoA c Maize ACCase enzym Maize acetyl CoA c Potato pollen cell Human gene express H. pylori GHPO 131

resp

EST clone HK650 Human hypoxia

Adenovirus pACTSG2 Adenovirus SCAR.RG C. elegans inhibit Encodes fibrinogen

Adenovirus pACSG2S Callosellasma rhod

DNA encoding a Bac Black Creek Canal

Human coxsackievir

Human coxsacklevir Enterococcus faeca

Genomic DNA encodi

Sh2-mlRev6 gene (s Shrunken-2 gene va Wild-type shrunken

Aminopeptidase 012 Aminopeptidase 012

Human OVCAl tumour

Enterococcus faeca Human OVCA2 tumour

Human type IV coll

Human secreted pro Breast cancer mamm MMTV env protein n Partial human comp

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

264507860117

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Result š

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New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for prophylactic or therapeutic treatment
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X13369
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A3 maize ACCase cD
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Acetyl-CoA-carboxy
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39.827 Million cell updates/sec
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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       This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species. L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and diagnosis of past or present LS infection.
                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity 100.
Matches 22; Conservative
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This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
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100.0%; Pred. No. 0.072;
ive 0; Mismatches 0;
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Zm41-A; male fertility; hybrid seed; transgenic plant; antisense;
ribozyme; male sterile; maize; Ms41-A; ds.
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Human; secreted protein; fusion protein; gene therapy; protein therapy, diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; osquitive disorder; schizophrenia; prostate; obesity; osteoclast; thynus; osteoplast; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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The invention relates to nucleic acid sequences (V84411 to V84633)
encoding human secreted proteins (W88534 to W88756). The secreted protein
encoding human secreted proteins (W88534 to W88756). The secreted protein
ce agenesca are deposated with the ATCC under deposit numbers ATCC
797919, 97974, 97975, 97976, 209007, 2090009, 2090010, 209011,
2090011, 209080, 209081, 209082, 209084, 209085, 209511. Host
cells comprising recombinant vectors containing the nucleic acid
cequences are used for the recombinant production of the secreted
cells comprising treating or ameliorating medical conditions e.g.
proteins. The polynucleotide and amino acid sequences are useful for are
useful for preventing, treating or ameliorating medical conditions e.g.
by protein or gene therapy. Pathological conditions can be also diagnosed
by determining the presence of mutations in the new polynucleotides.
Comprising the presence of mutations in the new polynucleotides.
Specific uses are described for each of the polynucleotides, based on
which tissues they are most highly expressed in, and include developing
comprising the diagnosis or treatment of cancer, neurodegenerative
disorders, developmental abnormalities and foetal deficiencies, blood
disorders, tumours, leukemias, diseases of the immune system, autoimmune
cischemic shock. Alzheimer's and cognitive disorders, schizophrenia,
crestenosis, prostate diseases, lymphomas, inflammation, allergies,
such as osteoporosis, arthritis or malignancies, diseases of testes, lung
cort thymus, dispersive/chockrine disorders, infections and AIDS. The
collypeptides are also useful for identifying their binding partners.
The present sequence represents a gene encoding a human secreted protein
contents of the present sequence represents and clone identification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW;
Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
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970S-0048901.
970S-0048917.
970S-0048963.
970S-0049019.
970S-0049019.
970S-0057627.
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97US-0057760.
97US-0057763.
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97US-0057774
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P-PSDB; W88721.
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06-JUN-1997;
06-JUN-1997;
05-SEP-1997;
05-SEP-1997;
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 73.6%; Score 16.2; DB 20; Length 951;
85.7%; Pred. No. 47;
iive 0; Mismatches 3; Indels 0;
                                                      Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoms; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsety; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                             Human secreted protein gene 126 clone HELGH31.
                                                V59636 standard; DNA; 1291 BP.
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9705-0043578.
9705-0043580.
9705-0043670.
9705-0043671.
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970S-0040336.
970S-0040626.
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97US-0047586.
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97US-0040333
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97US-0047503
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97US-0047582
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97US-00475
97US-00475
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23-MAY-1997;
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RESULT
V59636/c
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209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Pc portion (e.g. v59501) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V95311.V59012; amino acid sequences WW7711.W75056) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V5911 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
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                                                                                                                                                                                                                                                                                                         DB 19; Length 1291;
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Pred. No. 48;
0; Mismatches
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97US-0050359.
97US-0053344.
97US-0053377.
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Best Local Similarity 85.7%;
Matches 18; Conservative
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20-JUN-1997;
22-JUL-1997;
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Rosen CA;
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Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM
Kyaw H, Lafleur DW, Moore PA, Ni J, Olsen HS,
Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
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                                                                                        97US-0047614.
97US-0047615.
97US-0047617.
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P-PSDB; W74854.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence encodes a maize acetyl-CoA-carboxylase (ACCase, BC-6.4.1.2) fragment. The enzyme catalyses the formation of malonyl-CoA from acetyl-CoA and bicarbonate, and requires a biotin prosthetic group for activity. The enzyme is inhibited by several herbicides (e.g. fluazifop and sethoxydim) in monocotyledons. The sequence is a 2-kb EcoRI fragment of phage lambda-gtll clone 15-14, isolated from a maize inbred Al88 seedling cDNA library by
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                 probe; transcarboxylase active site; biotin binding site; screening; cassette; antisense; promoter; transit peptide; plasmid; tissue-specific gene expression; herbicide resistance; oilseed; oil content; transgenic plant; crop improvement; ss.
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/product= Transcarboxylase active site region
59..70
                                            Length 1473;
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   G; 498 T; 0 other;
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                                               DB
                                              Score 16.2; DE
Pred. No. 49;
0; Mismatches
                                                                                                                                                                                                                                                                                                                           acetyl-CoA-carboxylase; fluazifop;
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1770..1946
/*tag= a
      ● Sequence 1473 BP; 622 A; 232 C; 121
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88US-0269584.
90US-0538674.
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85.7%;
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                                                                            Conservative
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Best Local Similarity
Matches 18; Conserv
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10-NOV-1988;
18-JUN-1990;
21-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1996
                                                                                                                                                                                                                                                                       07-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MA,
DL;
                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays.
                                                                                                                                                                                                                                             T17111;
                                                                                                                                                                                                                                                                                                                                Maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wyse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A 2 kb EcoRI fragment (T39904) of lambda clone #15-14 includes a portion of a maize acetyl CoA carboxylase (ACCase) gene located at bases 2883 to 83 from the 3' stop codon. Clone #15-14 was isolated from a lambda gtll cDNA library of maize inbred A188 seedlings by screening with maize ACCase antiserum. Other ACCase DNA fragments (see also 79906-16) and a complete cDNA (T39905) coding ACCase isolated. ACCase DNA can be incorporated into a vector and used to increase the herbicide tolerance or oil
                                                                                                                                                                                                                                                                                                         Gaps
promoter, e.g. a cauliflower-mosaic virus 35S promoter or nopaline-synthase promoter, and N-terminal maize chloroplast transit peptide sequence in a plasmid vector for high-level tissue-specific gene expression, to confer herbicide resistance and/or alter the oil content of the plant, or to increase the plant Accase yield, so that the crystallized enzyme may be used to screen and identify other herbicides that bind to and inhibit the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding maize acetyl coenzyme A carboxylase gene - used for prodn. of plants with herbicide tolerance or altered oil content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetyl CoA carboxylase; ACCase; herbicide tolerance; cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil; oilseed; maize; corn; SS.
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                           Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     content of a transgenic plant, or used to produce ACCase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Somers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2001 BP; 546 A; 406 C; 494 G; 554 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize acetyl CoA carboxylase cDNA clone EcoRI fragment
                                                                                                                                                                                         Sequence 2000 BP; 546 A; 406 C; 494 G; 554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lutz SM,
                                                                                                                                                                                                                                                                                                            <u>ښ</u>
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Pred. No. 51;
0; Mismatches
                                                                                                                                                                                                                                                                                   Pred. No. 51;
); Mismatches
                                                                                                                                                                                                                                                                  Score 16.2; I
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gronwald JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 77; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                            22
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|larity 85.7%;
|Conservative
                                                                                                                                                                                                                                                                     73.68;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0417089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T39904 standard; cDNA; 2001
                                                                                                                                                                                                                                                                                                                                                                                     2 gttggatcacaagatttgata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gengenbach BG,
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterologous systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays line A188.
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Wvse DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T39904;
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Mycobacterium sp.; internal sequence; intein; immature; gyrase; protein splicing; precursor; gyrA; ss.
                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterial DNA gyrase precursor protein - and polypeptide(s) corresponding to mycobacterial DNA gyrase intein sequences
                                                                                                            M. leprae gyrA precursor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Pages 33-34; 55pp; French.
                                    T64683 standard; DNA; 3822 BP.
                                                                                                                                                                         Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                              WPI; 1997-247976/23.
                                                                                                                                                                                                                                                                                                                        Cole S, Fsihi H;
                                                                                                                                                                                                                                                                                                                                                              P-PSDB; W15078
                                                                                                                                                                                                                                                17-OCT-1995;
                                                                                                                                                                                                                                                                        17-0CT-1995;
                                                                                    17-MAR-1998
                                                                                                                                                                                                FR2739859-A1
                                                                                                                                                                                                                       18-APR-1997.
                                                           T64683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
            RESULT 11
                         r64683
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                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present DNA sequence is a 2kb EcoRI fragment of lamda clone #15-14 including a portion of a maize acetyl CoA carboxylase (ACGSse) gene located at bases 2883 to 83 from the 3' stop codon. AcCase is involved in fatty acid synthesis and is the target of the specified herbicides. Transformation of plants with ACGSse imparts resistance to cyclohexanedione and aryloxyphenoxypropanoic acid herbicides and alter the oil content. The ACGSse DNA is also used as source of probes and primers for the identification of transgenic plants; in marker-assisted plant selection and for restriction fragment length polymorphism mapping, used for high-energy animal feed and high-fiber, low-fat human food and in genetic dissection of the groat oil trait.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oil content
                                                                                                                                                         EcoRI fragment of lamda clone #15-14 with maize ACCase gene portion.
                                                                                                                                                                                              maize acetyl CoA carboxylase; ACCase, herbicide; plant oil content;
marker-assisted plant selection; groat oil trait;
restriction fragment length polymorphism mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Somers
                                                                                                                                                                                   Herbicide resistance; gene modification; lamda clone #15-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rines HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 2001 BP; 546 A; 406 C; 494 G; 554 T; 1 other;
                                                                                                                                                                                                                                  high-energy animal feed; low-fat human food; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 10; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Groh S, Kianian SF,
                                                                                                                                                                                                                                                                                                                                                                                                          US DEPT OF AGRICULTURE. EGLI M A. GROH S.
22
          249816 standard; DNA; 2001 BP
                                                                                                                                                                                                                                                                                                                                    99WO-US14022.
                                                                                                                                                                                                                                                                                                                                                           98US-0090240
98US-0091640
2 gttggatcacaagatttgata
                                                                                                                                  18-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                              KIANIAN S F.
PHILLIPS R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147205/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SOME/) SOMERS D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RINES H W.
                                                                                                                                                                                                                                                                                  W09967367-A1.
                                                                                                                                                                                                                                                                                                                                   22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                           22-JUN-1998;
02-JUL-1998;
                                                                                                                                                                                                                                                                                                           29-DEC-1999
                                                                                                                                                                                                                                                             Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Egli MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                             (KIAN/) H
(PHIL/) H
(RINE/)
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(EGLI/)
                                                                                                           249816;
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                                                                       249816
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95FR-0012162. 95FR-0012162.

(first entry)

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This DNA, isolated from Mycobacterium leprae, encodes a precursor (immature) gyrase protein from which an "intein" (see W15074) is excised during maturation. The gyrase and its coding sequence are useful to fabricate products that alter the maturation of proteins essential for the development of infectious agents by altering the protein splicing of precursor polypeptides of the proteins. The inteins encoded by the gyrapersors products in Flavescens, M. gordonae and M. kansasii are used: (a) to modify the genome of a eukaryotic cell that lacks endogenous biological activity identical to that of the polypeptide; (b) to replace a copy of a gene present in a recipient genome by integration of a gene different from that where the integration takes place; and (c) for targetted insertion of a foreign DNA sequence into a selected site in the genome of a eukaryotic cell not containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3822 BP; 843 A; 899 C; 1092 G; 988 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.2; DE
Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     specific cleavage sites of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2334 gttggatcagatgatttgtta 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 gttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q42933 standard; DNA; 4346 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.6%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A3 maize ACCase cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Gaps 0;

0;

Indels

. 3;

Ouery Match 73.6%; Score 16.2; DB 21; Best Local Similarity 85.7%; Pred. No. 51; Agtches ,18; Conservative 0; Mismatches 3;

2 gttggatcacaagatttgata 22

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Length 2001;

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902 gttggatgacaagagttgtta 922

T39905 standard; cDNA; 7470 BP

RESULT 13

139905

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The sequence is trans of the As accept board carboxylase (Access) CDNA maize clone which can be used to probe plant DNA to isolate other such clones. It may be used with plant regulatory sequences to produce expression cassettes for Accase. These cassettes are used to transform plants to downregulate prodn. Of Accase. This can alter the composition of seeds or other plant parts, e.g. enabling oil-bearing plants such as oliseed rape, sufflower or olipalm, having a lower or modified oil content to be produced. It can be used to form expression cassettes for overexpression of Accase. leading to prodn. Of plants with an increased oil content. It may also be used to recover the Accase gene promoter. This can be used to generate RNA in a tissue-specific or developmentally regulated manner, and this RNA used to inhibit Accase expression. Monocotyledonous plants can be made resistant to grass-weed herbicides such as fluazifop and alkylketones by transforming with cassettes adapted to express Accase. This is achieved by overexpression of monocot Accase, expression of dicot Accase (which is relatively tolerant to these herbicides used to destroy weeds growing between the plants. This allows the overall applien. Of herbicides used to destroy weeds growing between the plants. This allows the overall applien. Of herbicide without effecting the crop, and is also useful where there has been short term carryover of herbicide from the previous crop. Using the method, weeds such as wild oats may be controlled, and the farmer is given extra options to obtain an improved sitable crops are maize, wheat and harley. Chaaper or more effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of the A3 acetyl coA carboxylase (ACCase) cDNA
      Acetyl coA carboxylase: ACCase; probe; expression; oil content; lower; modified; increased; oilseed rape; sunflower; resistant; resistance; grass-weed herbicides; fluazifop; alkylketones; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA clones for use in probing plant DNA - comprise maize acetyl coenzyme-A carboxylase gene flanked by heterologous DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4346 BP; 1239 A; 829 C; 1064 G; 1213 T; 1 other
                                                                                                                                                                                                    /*tag= a
/note="ACcase"
1875..1878
/*tag= b
/note= "GAN encodes Glu or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suitable crops are maize, wheat and barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ICIL ) ICI AUSTRALIA OPERATIONS PTY LTD. (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whitfeld PR;
                                                                                                                                                      Location/Qualifiers
3..3947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 3; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            92WO-GB02205.
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                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-197061/24.
                                                                               wheat; barley; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; R36781
                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1992;
                                                                                                                                                                                                                                                                                                                            WO9311243-A.
                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1993
                                                                                                                        Zea mays.
                                                                                                                                                                 Key
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A CDNA sequence (T39905) codes for maize acetyl CoA carboxylase (ACCase) (W05590), an enzyme that plays a central role in fatty acid biosynthesis and accumulation in plants and seeds. The complete sequence was deduced from cDNA clone #18-5, obtd. from a lambda gtll cDNA library of maize inbred A188 seedlings, and from PCR amplifications (see also T39918-23). Genomic ACCase DNA frommerts have also been isolated (see also T39906-16). ACCase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragments have also been isolated (see also 739906-16). Accase Dr can be incorporated into a vector and used to increase the herbicide tolerance or oil content of a transgenic plant, or used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding maize acetyl coenzyme A carboxylase gene – used for prodn. of plants with herbicide tolerance or altered oil content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7470;
                                                                                                                                                                                                                                                                                                                                                                                    Somers DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                 Acetyl CoA carboxylase; ACCase; herbicide tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
                                                                                                                                                                                                                                                                                                                                                                                    Gronwald JW, Lutz SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071
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Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to produce ACCase in heterologous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 78-80; 131pp; English.
                                                                                                                                                                  Location/Qualifiers
37..7014
/*tag= a
                                                                                                                                                                                                 /*tag= a
/EC_number= 6.4.1.2
                                                        Maize acetyl CoA carboxylase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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85.7%;
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                            (first entry)
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Best Local Similarity 85.78
                                                                                                                                                                                                                                                                                                                                                                                  Gengenbach BG,
                                                                                                              oilseed; maize; corn; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-465030/46.
                                                                                                                                       Zea mays line A188.
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                                                                                                                                                                                                                                         WO9631609-A2
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                            23-JAN-1997
                                                                                                                                                                                                                                                                    10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                 Egli MA,
Wyse DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V29317;
T39905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V29317
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Gaps

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73.6%; Score 16.2; DB 14; Length 4346; 85.7%; Pred. No. 55; Live 0; Mismatches 3; Indels 0;

Query Match
Best Local Similarity 85.7*
Matches 18; Conservative

2 gttggatcacaagatttgata 22

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Zea mays.

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Accase is involved in farty acid synthesis and is the target of the specified herbicides. Transformation of plants with Accase imparts resistance to cyclohexanedione and aryloxyphenoxypropanoic acid herbicides and alter the oil content. The Accase DNA is also used as source of probes and primers for the identification of transgenic plants; in marker assisted plant selection and for restriction fragment length polymorphism mapping, used for high-energy animal feed and high-fiber, low-fat human food and in genetic dissection of the groat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present cDNA sequence encodes maize acetyl CoA carboxylase (ACCase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oll content
                                                                                                                              maize acetyl CoA carboxylase; AcCase; herbicide; plant oil content; marker-assisted plant selection; groat oil trait; restriction fragment length polymorphism mapping; high-energy animal feed; low-fat human food; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7470 BP; 2119 A; 1430 C; 1843 G; 2071 T; 7 other;
                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "Maize acetyl CoA carboxylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.6%; Score 16.2; DB 21;
85.7%; Pred. No. 58;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips RL,
                                                                                                              Herbicide resistance; gene modification;
                                                                                                                                                                                                                                                                  Location/Qualifiers
37..7014
                                                                          Maize acetyl CoA carboxylase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Fig 13; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Egli MA, Groh S, Kianian SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MINU ) UNIV MINNESOTA.
(USDA ) US DEPT OF AGRICULTURE.
(EGLI/) EGLI M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 2 gttggatcacaagatttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US14022
                                                                                                                                                                                                                                                                                                                                                              /*tag= b
7014..7470
/*tag= c
                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIANIAN S F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DEPT OF
EGLI M A.
GROH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; Y44687
                                    18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                          W09967367-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oil trait
                                                                                                                                                                                                                                Zea mays.
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(PHIL/)
(RINE/)
(SOME/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GROH/)
249820;
                                                                                                                                                                                                                                                                                                                                              5'UTR
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This cDNA encodes a maize ACCase enzyme. This can be used in a method of preparing an herbicide resistant corn plant which comprises crossing a first corn plant to a second corn plant so as to yield a progeny plant, where the first corn plant comprises at least 1 herbicide resistant allele which is not allelic to the herbicide resistant allele present in the first plant. The herbicide resistant corn plants are prepared using Acc1 and Acc2 gene combinations which impart cylcohexanedione (CHD) or aryloxyphenoxypropanoic acid (APA) herbicide tolerance to the corn plant. The methods are used to impart CHD and APA herbicide tolerance to corn plants and to produce CHD or APA herbicide tolerant Zea mays (corn) homozygous or heterozygous for Acc1 and homozygous or heterozygous for Acc2 and homozygous or heterozygous for Acc2. The methods can also be used to impart tolerance to a corn plant to an agent which inhibits accetyl CoA carboxylase, selected from 20.2.4-dichlorophenyl) perhyddoindolizine-2.4-dione, 3 isopropyl-6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                        ACCase; maize; herbicide resistant; corn plant; tolerance; Accl; Acc2; cylcohexanedione; CHD; aryloxyphenoxypropanoic acid; APA; enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herbicide resistant corn plants · prepared using Accl and Acc2 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071 T; 7 other;
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85.7%; Pred. No. 58;
ive 0; Mismatches 3;
                                                                                                                                                                                                                    /*tag= a //transl_except= (pos:4339..4341, //transl_except= (pos:4456..4458, //transl_except= (pos:4359..4461, /product= "ACCase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marshall LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Fig 3A-E; 112pp; English.
                                                                                                                                                                                    Location/Qualifiers
37..7014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lutz SM,
                                                        Maize ACCase enzyme encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wyse DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3972 gttggatgacaagagttgtta 3992
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gengenbach BG,
, Vandee KL, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-207043/18.
P-PSDB; W56736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                          WO9808963-A1
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                30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                05-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somers DA,
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Egli MA,

Somers DA;

Rines HW,

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Gaps

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Indels

3972 gttggatgacaagagttgtta 3992

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249820 standard; cDNA; 7470 BP.

RESULT 15 Z49820

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Length 7470;

Search completed: March 27, 2001, 08:23:02 Job time: 5304 sec

us-09-380-826a-7.rng

Appli Appli Appli Appli Appli Appli Appli Appli

Sednence Sed

Sequence Sequence Sequence

ALIGNMENTS

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Sequence 1. Application US/08014326

Sequence No. 5498544

GENERAL INFORMATION:
APPLICANT: Gengenbach, Burle G.
APPLICANT: Somers, David A.
APPLICANT: Growald, John W.
APPLICANT: Egil, Margaret A.
APPLICANT: Egil, Margaret A.
APPLICANT: Lutz, Shiela M.
TITLE OF INVENTION: Method and An Acetyl CoA Carboxylase
TITLE OF INVENTION: Alteration in Oil Content of Plants
NUMBER OF SEQUENCES: 4
CORRESPONDENCES 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5498544west Center
CITY: Minneapolis
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/014,326
FILING DATE: 05-FEB.1993
                              US-08-204-6568-1
US-08-204-6568-3
US-08-204-6568-5
US-08-470-702-1
US-08-470-702-2
US-08-470-702-3
US-08-470-702-4
US-08-467-831-2
US-08-467-831-3
US-08-467-831-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR AFFLICATION UNBER: US 07/538,674
FILING DATE: 18-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUBER: US 07/269,584
FILING DATE: 10-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: KOWAICHY, KATHERINE M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 600.258-US01
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHANE: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,462
FILING DATE: 21-UL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                 COMPUTER READABLE FORM:
                                   USA
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ZIP: 55402
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STATE:
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Patent No. 5256642
Patent No. 5472939
Patent No. 5256642
Patent No. 5472939
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26.799 Million cell updates/sec
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Sequence 1, Appli
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Sequence 5, Al
Sequence 5, Al
Sequence 14,
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Sequence 4, Al
Sequence 3, Al
Sequence 3, Al
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                                                                                                                  March 27, 2001, 08:19:23; Search time 132.3 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-485-241-1
US-08-874-162-1
US-08-399-986B-3
US-08-399-986B-3
US-08-399-986B-1
US-08-493-754A-3
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US-08-684-862-8
US-08-792-055-1
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US-08-119-361-4
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                                                                                                                                                                                                                                                                                                          280836 segs, 80580151 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                  METHODS AND AN ACETYL COA CARBOXYLASE GENE
FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                            DB 1; Length 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATE: US/08/417,089
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
             MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: 2 kb fragment of lambda clone #15-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                         73.6%; Score 16.2; I
85.7%; Pred. No. 20;
Live 0; Mismatches
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85.7%; Pred. No. 20;
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Patent No. 6146867
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Patent No. 6069298
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                                                                                                                                                                                                                                    42 GTTGGATGACAAGAGTTGTTA 62
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US-08-417-089-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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Gronwald, J. W.
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 85.7
Matches 18; Conservative
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TITLE OF INVENTION: FOR
TITLE OF INVENTION: OIL
NUMBER OF SEQUENCES: 11
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: E911, M. A. APPLICANT: Lutz, S. M. TITLE OF INVENTION: METH NUMBER OF SEQUENCES: 11
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                              Best Local Similarity
Matches 18; Conserva
linear
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TOPOLOGY:
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APPLICANT:
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STATE: M
COUNTRY:
                                                                     US-08-014-326-1
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APPLICANT:
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                                                                                                                            Query Match
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Sequence 1, Application US/08244537
Sequence 1, Application US/08244537
Sequence 1, Application US/08244537
Sequence 1, Application US/08244537
SENERAL INFORMATION:
APPLICANT: ASHTON, ANTHONY R.
APPLICANT: WHITFELD, PAUL R.
TITLE OF INVENTION: MAIZE ACETYL COA CARBOXYLASE ENCODING
TITLE OF INVENTION: DNA CLONES
TITLE OF INVENTION: DNA CLONES
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                                                                                                APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
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FILING DATE: 18-AUG-1994
CLASSIFICATION: 800
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                                                                                                                                                                                                                  APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                       SYSTEM: DOS
FastSEQ Version 2.0
                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/417089
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REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
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COUNTRY: U.S.A.
ZIP. 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.6%;
85.7%;
: Diskette
IBM Compatible
                                                                                                                                                                                                   FILING DATE: 05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001 base pairs
                                                                             CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN D.
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                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
Matches 18; Conserv
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                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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APPLICANT: Goltry, Kristin L.
APPLICANT: Greenberger, Joel S.
TITLE OF INVENTION: DETERNING EXPOSURE TO IONIZING RADIATION
TITLE OF INVENTION: AGENT WITH PERSISTENT BIOLOGICAL MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7470;
                                                                   TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COA
                                                                                                                                                                   E: Schwegman, Lundberg, Woessner & Kluth, P.A. P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 23;
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600.318US3
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; Sequence 14, Application US/08602145
; Patent'No. 6025336
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APPLICATION NUMBER: 08/117089 ·
FILING DATE: 05-APR-1995
APPLICATION NUMBER: 08/014326
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APPLICATION NUMBER: 07/917/457
FILING TANGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/917462
FTLING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 612-373-6900
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,4
                                            Sronwald, J. W.
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Best Local Similarity 85.77
Matches 18; Conservative
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EDNESS: single
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                                                                                                                                                                                                           Minneapolis
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US-08-695-651-5
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                                                                                                                                                                                                                                                                      ZIP: 55402
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STREET: 30
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                                            APPLICANT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,089
INFORMATION FOR SEQ ID NO: 5:
PRIOR APPLICATION DATE:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
FILING DATE:
ATPORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
RECISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 203094/SEE 36663/UST
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (202) 861.3000
TELEX: 6714627 COSH
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4345 base pairs
LENGTH: 4345 base pairs
TYPE: Nucleic acid
STRANDEDNESS: both
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Pred. No. 22;
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85.7%; Pred. No. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 5, Application US/08695651
; Patent No. 6146867
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                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-08-244-537-1
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US-08-417-089-5
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Best Local Similarity 85.7%;
Matches 18; Conservative
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LENGTH: 7470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gengenbach, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 gttggatcacaagatttgata
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Best Local Similarity 85.7
Matches 18; Conservative
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TITLE OF INVENTION: METH
TITLE OF INVENTION: FOR
TITLE OF INVENTION: OIL
UNDBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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APPLICANT: Elliott, Luanne
APPLICANT: Elliott, Luanne
APPLICANT: Kslazek, Thomas G.
APPLICANT: Nichol, Stuart T.
APPLICANT: Morzunov, Sergey
APPLICANT: Morzunov, Eugeny
TITLE OF INVENTION: The Black Creek Canal Hantavirus and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSE: NEBDLE & ROSENBERG, P.C.
ADDRESSEE: NEBDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, N.E., Suite 1200
                                                                                                                                                                                                                                                                            Score 15.6; DB 1; Length 1096;
Pred. No. 37;
0; Mismatches 4; Indels 0
                                                                                                                                             LOCATION: 144 to 841
CTHER INFORMATION: the coding region shown in (2)(ix)(B)
CTHER INFORMATION: codes for the protein of SEQ ID NO: 3
US-08-684-862-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,055
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,361
FILING DATE:
ATTOMNEY/AGENT INFORMATION:
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                                                                             MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08792055
Patent No. 5853980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                  1 tgttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                          112 TGTAGTATCACAAGGTTTGCTA 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (404) 688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISICS:
LENGTH: 1989 base pairs
                                                                                                                                                                                                                                                                                Ouery Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
LENGTH: 1096 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
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MEDIUM TYPE: Floppy
                     nucleic acid
EDNESS: single
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OPERATING SYSTEM:
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STREET: 12, .
CITY: Atlanta
cTATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                              TOPOLOGY: linear
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                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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APPLICANT: Bach, Alfred
APPLICANT: Hillen, Heinz
APPLICANT: Hillen, Heinz
APPLICANT: Hillen, Siegfried
TITLE OF INVENTION: No. 5759541el Proteins, the Preparation and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                               COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,145
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAKX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 2036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM AT-compatible, 80286 processor OPERATING SYSTEM: MS-DOS version 5.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
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Pred. No. 31;
0; Mismatches
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APPLICATION NUMBER: 07/966,040
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: FCT/EF91/01361
FILING DATE: 19-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-684-862-8/c
; Sequence 8, Application US/08684862
; Patent No. 5759541
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                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
      20007-5109
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CORRESPONDENCE ADDRESS:
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US-08-874-162-1/c
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                                    70.9%; Score 15.6; DB 2; Length 1989; 81.8%; Pred. No. 39;
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                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
TITLE OF INVENTION: Materials and Methods for Increasing
TITLE OF INVENTION: Corn Seed Weight
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Materials and Methods for Increasing
Corn Seed Weight
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                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                            0; Mismatches
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81.8%; Pred. No. 46
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Patent No. 5650557
GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
                                                                                                                                                                                                                                                           Sequence 1, Application US/08299675 Patent No. 5589618
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NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/CDOCKET UNEMBER: UF14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                  288 TGTTGGATCAACAGATTTTGTA 267
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MOLECULE TYPE: DNA (genomic)
US-08-299-675-1
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 18; Conservative
                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2421 N.W. 41SE
CITY: Gainesville
STATE: E.
COUNTRY: USA
2.IP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 904-375-810
TELEFAX: 904-372-5800
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CLASSIFICATION: 435
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                    Query Match
Best Local Similarity
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US-08-299-675-1/c
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                                                                            Matches
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Patent No. 5872216
GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
TITLE OF INVENTION: Materials and Methods for Increasing
TITLE OF INVENTION: Corn Seed Weight
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,241
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5: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 46;
0; Mismatches
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81.8%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION. CONTROL ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,675
FILING DATE: 1-SEP-1994
CLASSIFICATION: 800
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FILING DATE: 13-JUN-1997
                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) US-08-485-241-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 7745 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.9°
Best Local Similarity 81.8°
Matches 18; Conservative
                                                           STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                             Gainesville
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STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Gaps

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Godwin, Andrew K.
VENTION: No. 5801041el Gene Associated with Suppression
VENTION: of Tumor Development
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TITLE OF INVENTION: No. 5821338el Gene Associated with Suppression
TITLE OF INVENTION: of Tumor Development
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1016;
                                                      Score 15.2; DB 1; Length 1016; Pred. No. 57; 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street CITY: Philadelphia STAIE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/493,754A FILING DATE: 2JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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Pred. No. 57;
0; Mismatches
                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08493754A
Patent No. 5821338
GENERAL INFORMATION:
GAPPLICANT: Godwin, Andrew K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-399-986B-1/c
; Sequence 1, Application US/08399966B
; Patent No. 5801041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830 TTGGGTCTCAAGAATTGATA 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4040
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                     830 TTGGGTCTCAAGAATTGATA 811
                                                          69.1%;
85.0%;
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85.0%;
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                                                                                                                                             3 ttggatcacaagatttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                  Ouery Match
Best Local Similarity 85.07
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: GODWIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                    RESULT 14
US-08-493-754A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-493-754A-3
US-08-399-986B-3
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APPLICANT: GODWIN, Andrew K.
TITLE OF INVENTION: No. 5801041el Gene Associated with Suppression
TITLE OF INVENTION: Of Tumor Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7745;
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COUNTR: c.

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATENTIN PRESENTED: PCDS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,986B
FILING DATE: 06-MR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hagan. Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
TELEFUNDE: (215) 563-4100
TELEFUNDE: (215) 563-4100
TELEFUNDE: (215) 563-404

INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.9%; Score 15.6;
81.8%; Pred. No. 46;
                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,675
FILING DATE: 1-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R. R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: UF-146C1D1
TELECOMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFPHONE: 352-375-8100
  US 08/485,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08399986B Patent No. 5801041
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                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-874-162-1
                                                                                                                                                                                                                                                                       TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
    APPLICATION NUMBER:
                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-08-399-986B-3/c
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Gaps

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CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman STRET: 1601 Market Street
CITY: Philadelphia STATE: PA
COUNTR: Philadelphia STATE: PA
COUNTR: USA
CONDUTR: 19103-2307
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: 27,643
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Pattick J.
REGISTRATION NUMBER: 27,643
TELEPHONE: (215) 563-4044
INPORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (Genomic)
HYPOTHETIAL: NO
WANTI-SENSE: NO
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Gaps ó Query Match 69.1%; Score 15.2; DB 1; Length 2182; Best Local Similarity 85.0%; Pred. No. 62; Matches 17; Conservative 0; Mismatches 3; Indels 0 3 ttggatcacaagatttgata 22 |||| || || || || || || || 1996 TTGGGTCTCAAGAATTGATA 1977 ò

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Search completed: March 27, 2001, 08:19:25 Job time: 5152 sec

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9b_est46:*;

9b_est46:*;

9b_est49:*;

9b_est51:*;

9b_est51:*;
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                                                                         March 27, 2001, 07:38:25; Search time 2517.78 Seconds (without alignments) 61.230 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                  7991742 seqs, 3503743858 residues
                                                                                                                                                               1 tgttggatcacaagatttgata 22
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Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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190: 191: 192: 193:

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130: qb_est6:*

131: qb_est6:*

131: qb_est6:*

132: qb_est6:*

133: qb_est6:*

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135: qb_est76:*

136: qb_est8:*

141: qb_est8:*

142: qb_est8:*

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147: qb_est8:*

156: qb_gss:*

157: qb_gss:*

158: qb_gss:*

159: qb_gss:*

150: qb_gs
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			To post top	•		SUMMARIES	
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υ		8.8	85	527	37	AV520789	AV520789 AV520789
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ט נ		. 4.	83	934	191	CNSO2BWA	AL190387 Tetraod
Ö		7.8	80	009	138	BF006444	BF006444 EST4345
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)		7.4	79	529	158	AQ497779	AQ497779 HS_506
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O.		17.2	78.	425	15	AI049911	A1049911 all301103 A0595814 HS 213
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O		17.2	7 00	579	77	86/515	BO/313 122F11311 AT777095 EST258(
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ט		17.2	7.8	619	97	AW963686	AW963686 EST3757
υ		17.2	78	.680	17,	B57784	B57784 CIT-HSP
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		17.2	78	406	2,5	CNSOZBDN	AL291166 Tetrac
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t	37	16.8	76	238	34	AV313332	AV313332 AV3133
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	•	16.8	7	296	14	5 T20362	T20352 5C01908
O	40	16.8		395	2 6	AW943911 AM487226	AW487226 81727
	c	16.8 16.8	- 1	432	15	7 A0449764	AQ449764 50000
	3 ~	16.8	26	446	24	AI761541	AI761541 w161f0
	. =+	16.8		450	13	3 BF002933	BF002933 7951C
υ	45	16.8	92	464	12	5 AQ332265	AQ33220 HS_0
						ALIGNMENTS	
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7	DEFINITION		ng e	CDNA CL	clone	FB034f09F 3', mRI	dneuce.
AC	ACCESSION VERSION		AV532040 AV532040.	1 GI:8	169232	23	
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90.9%;
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Matches 20; Conservative
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 361)

Asamizu, E., Nakamura; Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana; Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="ecotype_Columbia"
/db_xref="taxon:3702"
/clone="vCVDH08"
/clone_lib="versailles-vC"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5 days old"
/dever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                    The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisazazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Arabidopsis thaliana flower buds Columbia"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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Contact: Desprez T., Amselem J., Chiapello H., Rouze
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cedex, France
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
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Route de Saint-Cyr, 78026 Versailles
Email: thierry@versailles.inra.fr.
Location/Qualifiers
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/clone="FB034f09F"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Columbia"
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90.9%;
Arabidopsis thaliana
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226559.1 GI:404227
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Best Local Similarity 90.9
Matches 20; Conservative
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 490)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Arabidopsis thaliana Above-ground organ from two to six-week old plants Columbia"
/tissue_type="Above-ground organ from two to six-week old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV520789 Arabidopsis thaliana aboveground organs two to six-week and Arabidopsis thaliana cDNA clone APZ32g06F 3', mRNA sequence. AV520789.1 GI:8680316
                                                      Gaps
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                                                                                                                                                                                                                                                                                          29-SEP-2000
                                                                                                                                                                                                                                                                                  AB038725 490 bp mRNA EST 29-SEP-2000 AB038725 Arabidopsis thaliana Above-ground organ from two to six-week old plants Columbia Arabidopsis thaliana cDNA clone AP230903_£ 3', mRNA sequence.
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  Length 394;
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  DB 147;
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/organism="Arabidopsis thaliana"
Score 18.8; DE
Pred. No. 35;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Columbia"
/db_xref="taxon:3702"
/clone="APZ30903_f"
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AUTHORS TITLE

REFERENCE

MEDLINE

COMMENT

JOURNAL

source

FEATURES

BASE COUNT ORIGIN

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Unpublished (1999)
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NuDDA, National Institutes of Health
NIDDA, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@helix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC: see http://www.nisc.nih.gov).
Plate: 66 row: h column: 08
Seq primer: MJ3RPI reverse primer (ABI).
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/lab_host="SOLR (Stratagene)"
/note="Organ: testis; Vector: pBlueScript SK (Stratagene);
Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
day adult y(*) w(67c1]/Y males raised at 25oC. RNA
isolated using Trizol (Life Technologies) and a single
                                                                                                                                                           /note="vector: psporr; Site_1: Not!; Site_2: Sall; cDNA library was derived from untreated inflorescence tissue from Arabidopsis thaliana, columbia col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 pear of 4 - 7 moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Bouble-stranded cDNA was blunted, ligated to Sall adaptors , digested with NotI, size-selected, and cloned into the NotI and Sall sites of the pSPORT vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bs66h08.yl Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs66h08 5', mRNA sequence.
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/sex="male"
                                               /clone="701676626"
/clone_ilb="A. thaliana, Columbia Col-0, inflorescence-1"
/issue_type="inflorescence"
/dev_stage="4 - 7 weeks"
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Drosophila melanogaster testis expressed sequence tags
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0; Mismatches
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/db_xref="taxon:7227"
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Best Local Similarity
Matches 20; Conserv
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BE977618/C
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TITLE
JOURNAL
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Warabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudiocryledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 530)
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gillilland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyan, D., Tan, R.,
Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L.,
Turner, C., Krikorian, S., Elder, L. and Hanson, D.
Arabidopsis thallana Gene Expression MicroArray
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 527)

Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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701676626 A. thaliana, Columbia Col-0, inflorescence-1 Arabidopsis
thaliana cDNA clone 701676626, mRNA sequence.
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/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Arabidopsis thaliana aboveground organs two
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Tel: 877-577-2733
Fax: 314-427-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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/cultivar="Columbia Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/clone="AP232g06F"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 90.9
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
254C22 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Teleostei; Buteleostei; Neoteleostei; Burypterygii; Chenosquamata; Acanthomorpha; Bucanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodontidae; Tetraodontoidei; Tetraodontidae; Tetraodon. 1 (bases 1 to 934)

Neost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
round of Poly(A)+ selection using Oligotex (Qiagen). CDN library constructed using Stratagene ZAP-CDNA syntesis kit. Oligo dr-primed, size fractionated -1-6 kb, and directionally cloned at EcoRi and XhoI in Uni-ZAP XR. Pollowing a single round of amplification pBlueScript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be honored."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 934)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
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                                                                                                                                                                                                                                                                                                      Gaps
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/note="Genoscope sequence ID : C0AG254BB11SP1-end
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                                                                                                                                                                                                                                                          83.6%; Score 18.4; DB 138; Length 608; 95.0%; Pred. No. 59;
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/db_xref="taxon:99883"
/clone="254C22"
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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95.0%;
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Matches 19; Conservative
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/tissue_type="leaves and cotyledons"
/describe="liature of cotyledons from five days old
plants and leaves obtained from two weeks old plants.
/lab_host="E. coll strain SOLR"
/lab_host="E. coll strain SOLR"
/note="Vector: pBluescript SK +/-: Site_1: EcoRI: Site_2:
XhoI: cDNA was prepared from polyA+ enriched RNA from the
mixture of cotyledons of five days old plants and leaves
of two weeks old plants. The cDNA was directionally
ligated into the Uni-ZAP XR vector from Stratagene and
packaged using Glapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant lambda ZAP phage using Ex-Assist helper phage
and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Eabales; Fabaceae; Papilionoideae; Medicago.

1 (bases I to 600)
Fedorova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., Vance, C.P., Gonzales, M.B. and Ellis, L.
ESTS from Medicago truncatula leaves and cotyledons
Unpublished (2000)
Contact: Deborah A. Samac
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
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                                                                                                                                                                                           BF006444 600 bp mRNA EST 06-OCT-2000 EST434942 DSLC Medicago truncatula cDNA clone pDSLC-41315, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Minnesota name: MZ75482e TIGR sequence name: MTLBA56TK More information is available at: http://chrysie.tamu.edu/medicago seq primer: Sknod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 1.2e+02;
0; Mismatches 2; 1
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/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSLC-41J15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: debbys@puccini.crl.umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="DSLC"
                                                                                                                                                                                                                                                                                                        BF006444.1 GI:10706719
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                          840 TTGGAACACAAGATTTGATA 821
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90.5%;
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BF006254/c
LOCUS
DEFINITION 1
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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takaki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahishi, T., Yamanara, Y., Yamanishi, A., Yokota, T., Yoshida, K., Yamanara, T., Yamanata, M., Muramatsu, M. and Hayashizaki, Y. Riken Mouse ESTS (Konno, H., et al.)
AL Unpublished (2000).
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Science Center, Tensing Marking 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-resettc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Caninoi.p. Nishlyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 5510-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /...yours... ...a muscurds
/db_xref=taxon:l0090"
/clone="B020032C12"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
/tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.4; DB 126; Length
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_rype="leaves and cotyledons"
/dev_stage="mixture of cotyledons from five days old plants and leaves obtained from two weeks old plants"
/lab_host="E. col; strain SOLR"
/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: xhoi; cDNA was prepared from polyA+ enriched RNA from the mixture of cotyledons of five days old plants and leaves of two weeks old plants. The cDNA was directionally ligated into the Uni-ZPA RX vector from Strangene and packaged using Glapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                 Tracheophyta; Spermatophyta;
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                                                                                                                                                                                                                                                                                                    core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                   Vance, C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M275292e TIGR sequence name:
WTLAN47Tk More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: Sknod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                           Fedorova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., Gonzales, M. B. and Ellis, L. Gonzales, M. Ests from Medicago truncatula leaves and cotyledons Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                    Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/cultivar="genotype A17"
/db xref="taxon 3880"
/clone="pDSiC-40G21"
                                                                                                                                                                                                                 Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core eud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="DSLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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ilarity 90.5%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 633)
                                                                                                                                                                                         barrel medic.
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Mus musculus
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Best Local Similarity
Matches 19; Conserv
                                                                                                              BF006254.1
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BASE COUNT ORIGIN

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS

RESULT 10

g

вв288727/с

source

FEATURES

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Gaps

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Length 286;

and

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High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3687
Fax: (206) 616-3687
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 642 row: J column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula
Bukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 529)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gonzales, R.A., Bell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000) Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF082E04ST1F1034 Developing stem Medicago truncatula cDNA clone NF082E04ST 5', mRNA sequence.
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.
                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                         scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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/clone="Plate=642 Col=9 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 others
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Pred. No. 1.8e+02;
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99 c 109 g 165 t
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Location/Qualiflers
1. 529
/organism="Homo sapiens"
                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW695022.1 GI:7569784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ttggatcacaagatttgat 21
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Matches 18; Conservative
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Class: BAC ends
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AW695022/c
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COMMENT
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KEYWORDS
SOURCE
                                                     REFERENCE
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/strain="Rhabditiform larvae obtained from gerbils"
/db_zerf="texaon:6248"
/clone_lib="TBN95TW-SSR"
/lab_host="XL-1 Blue MRF" (Stratagene); Site_1:
/note="vector: Lambda Uni-2AP R (Stratagene); Site_1:
ECORI, Site_2: Xho! mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected duth larvae originally isolated
from experimentally infected dogs. cDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the ECORI site to the Xho! site. The library
has an unamplified titer of 1 x 10E5 pfu/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
average insert size of the unamplified library is 675 bp
(range, 100-1700)."
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                                                                                                                                                                                                                                                                                                                         McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colleagues of
                               BEST 16-AUG-2000 mRNA EST 16-AUG-2000 KSJ1007.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar WP:T19910.2 CE16413;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Longublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues
NIAID, NIH (tnutman@ihi.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 384.
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Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
                                                                                                                                                                                                                                 Strongyloides stercoralis.
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NIH MGC http://www.ncbi.nlm.nlh.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenin.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE283043 762 bp mRNA EST 13-JUL-2000 601101323F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3493829 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
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internodal stem segments"
149 c 133 g 203 t
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Plate: LLAM8541 row: n column: 06
High quality sequence stop: 661.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7380
                                                                                                                                                                                                    1. .674
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="RK082E045T"
/clone_lib="Developing stem"
/tissue_type="stem"
                                                                                                                                                                                                                                                                                                                              /dev_stage="Pooled developmental"
                                                                                                 Email: radixonenoble.org
Insert Length: 674 Std Error: 0.00
Plate: 082 row: E column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
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Mus musculus
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Best Local Similarity
Matches 18; Conserv
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//dev_stage="20 hours after germination initiation"
//dev_stage="20 hours after germination initiation"
//note="stage="20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores that had developed for 20 hours after richardii spores richardii spores
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Expressed sequence tags of CDNA clones from a C. richardii library
Unpublished (2000)
Contact: Roux SJ
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Fel: 512 471 4238
Fex: 512 232 34402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ceratopteris richardii.
Ceratopteris richardii
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Filicophyta;
Filicopsida; Filicales; Pteridaceae; Ceratopteris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE642809 837 bp mRNA EST 01-SEP-2000 Cri2_7_B04_SP6 Ceratopteris Spore Library Ceratopteris richardii cDNA clone Cri2_7_B04_5', mRNA sequence.
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Pred. No. 1.9e+02;
); Mismatches 1; Indels 0;
                                                                                                                                                                                                                                            Length 762;
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/db_xref="taxon:49495"
/dlone="Cri2__B04"
/clone_lib="Ceratopteris Spore Library"
/tissue_type="Gametophyte"
/cell_type="Spore"
providing samples: Gilbert Smith, NIH" 172 c 207 g 190 t
                                                                                                                                                                                                                                            DB 106;
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                                                                                                                                                                                                                                       Score 17.4; DB 100
Pred. No. 1.9e+02;
); Mismatches 1.
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Plate: Cri2_7 row: B column:
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94.78;
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Best Local Similarity 94.7%;
Matches 18; Conservative
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